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OM protein - protein search, using SW model

Run on: January 29, 2003, 13:24:07 (Search time 37 Seconds
(without alignments)
965.167 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444
Sequence: 1 MSRLALVGAALVSSACGG.....QRVLGLPGIIRVSRGVV 268

Scoring table: BLAST62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444	100.0	268	23 AAE18634	Human beta1a sodium channel
2	799.5	55.4	272	22 AAB62320	Rat sodium channel
3	799.5	55.4	272	22 AAB20371	Rat beta1 subunit, beta1
4	751	52.0	218	21 AAB36031	Rat beta3 subunit, beta3
5	751	52.0	218	22 AAB62326	Rat sodium channel
6	749	51.9	218	22 AAB50260	Novel human channel
7	263.5	18.2	1176	22 ABE22576	Novel human channel
8	258.5	17.9	159	21 AAB36020	Human beta3 subunit
9	258.5	17.9	195	22 AAM79212	Human protein SDO
10	258.5	17.9	215	21 AAB36002	Human beta3 subunit

11	258.5	17.9	215	22 AAB85206	Human novel sodium
12	258.5	17.9	215	23 ABB05689	Human signal trans
13	257.5	17.8	159	21 AAB36021	Rat beta3 subunit
14	257.5	17.8	191	22 AAB50245	Rat sodium channel
15	257.5	17.8	215	21 AAB36001	Rat beta3 subunit
16	257.5	17.8	215	22 AAB50243	Rat sodium channel
17	207.5	14.4	369	22 ABE22577	Novel human channel
18	139	9.6	206	22 ABE22575	Novel human channel
19	115.5	8.0	209	23 AAB80200	Human protein zero
20	115.5	8.0	209	23 AAB80192	Human protein zero
21	115.5	8.0	269	23 AAB80193	Human protein zero
22	115.5	8.0	269	23 AAB80194	Human protein zero
23	115.5	8.0	269	23 AAB80209	Human protein zero
24	114.5	7.9	159	23 AAB80207	Human protein zero
25	114.5	7.9	199	23 AAB80211	Human protein zero
26	114.5	7.9	199	23 AAB80213	Human protein zero
27	114.5	7.9	209	21 AAB94998	Human secreted pro
28	114.5	7.9	209	21 AAB80199	Human protein zero
29	114.5	7.9	209	23 AAB80201	Human protein zero
30	114.5	7.9	269	21 AAB99445	Human protein zero
31	114.5	7.9	269	21 AAB66194	Human protein of the inv
32	114.5	7.9	269	23 AAB80216	Human protein zero
33	114.5	7.9	269	23 AAB80217	Human protein zero
34	114.5	7.9	269	23 AAB80218	Human protein zero
35	114.5	7.9	269	23 AAB80219	Human protein zero
36	114.5	7.9	269	23 AAB80220	Human protein zero
37	114.5	7.9	269	23 AAB80221	Human protein zero
38	114.5	7.9	269	23 AAB80222	Human protein zero
39	114.5	7.8	159	23 AAB80223	Human protein zero
40	112.5	7.8	159	23 AAB80224	Human protein zero
41	112.5	7.8	199	23 AAB80225	Human protein zero
42	112.5	7.8	199	23 AAB80226	Human protein zero
43	110.5	7.7	215	20 AAB34467	Human channel-rela
44	110.5	7.7	215	21 AAB34468	Human channel-rela
45	110.5	7.7	215	21 AAB6752	Membrane-bound pro

ALIGNMENTS

RESULT 1	AAE18634	standard; Protein; 268 AA.
ID	AAE18634	
AC	AAE18634	
DT	17-MAY-2002	(first entry)
XX		
DB	Human beta1a sodium channel subunit protein.	
XX		
KM	Human, voltage gated sodium channel; VGSC; antisense therapy; arrhythmia;	
KW	gene therapy; neuropathic pain; epilepsy; anticonvulsant; analgesic;	
KW	chromosome 19.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..16
FT	Protein	/label= signal_peptide
FT	Region	17..268
FT		/label= Mature_beta1a_sodium_channel_subunit_protein
FT		243..262
FT		/note= "Hydrophobic carboxy terminal residues"
PN	WO200194414-A2.	
XX		
PD	13-DEC-2001.	
XX		
PF	06-JUN-2001; 2001WO-US18304.	
XX		
PR	07-JUN-2000; 2000US-294405P.	
PR	29-SEP-2000; 2000US-236664P.	
XX		

PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX Qln N, Codd E, D'andrea M;

XX WPI: 2002-179468/23.

XX N-PSDB; AAD29622.

XX New human voltage gated sodium channel (VGSC) beta-1A subunit useful
XX for identifying modulators of the functional human VGSC beta-1A
XX subunit, for treating neuropathic or chronic pain, epilepsy, and
XX arrhythmia.

XX Claim 15; Page 96-98; 98pp; English.

XX The invention relates to an isolated polynucleotide encoding a human
XX voltage gated sodium channel (VGSC) beta1A subunit protein. Human beta1A
XX sodium channel subunit proteins, nucleic acids and antibodies may be used
XX to screen and measure levels of human beta1A sodium channel subunit DNA,
XX RNA or protein, and to detect and type human VGSC beta1A sodium channel
XX subunit. Nucleotide sequences complementary to the human beta1A sodium
XX channel subunit encoding DNA can be synthesised for antisense therapy,
XX and nucleotide sequences are useful in gene therapy. The human beta1A
XX sodium channel subunit protein is useful for identifying modulators of
XX the functional human beta1A subunit, and such modulators of sodium
XX channel activity or compositions comprising them are useful for treating
XX neuropathic or chronic pain, epilepsy, and arrhythmia, which is measured
XX by a change in sodium channel activity. VGSC beta1A subunit is useful
XX for identifying modulators of functional human VGSC beta-1A subunit
XX which decreases the expression of sodium channel beta1A subunit in the
XX cells of the individual. The present sequence is human beta1A sodium
XX channel subunit protein. Human beta1A sodium channel subunit gene is
XX located on chromosome 19.

XX Sequence 268 AA;

Query Match 100.0%; Score 1444; DB 23; Length 268;
Best Local Similarity 100.0%; Pred. No. 1,1e-138;

Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMFTFKILICISCKRSEETAETETWTFR 60
DB 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMFTFKILICISCKRSEETAETETWTFR 60

QY 61 QKGTSEFVKILRYENEVQLLEDERFEGRVVWNGSGRTKLDLSIFITVTVYHSGDYE 120
DB 61 QKGTSEFVKILRYENEVQLLEDERFEGRVVWNGSGRTKLDLSIFITVTVYHSGDYE 120

QY 121 CHVYRLFFENYENTSVVKKIHIEVDKSGSACPTVTHRRARMDRQAVDRGTWL 180
DB 121 CHVYRLFFENYENTSVVKKIHIEVDKSGSACPTVTHRRARMDRQAVDRGTWL 180

QY 181 CAMPANRPOQRAEGSSPCPLQMLPFLSSPRGQSMVPHRRSGYRTQCLCHCMTS 240
DB 181 CAMPANRPOQRAEGSSPCPLQMLPFLSSPRGQSMVPHRRSGYRTQCLCHCMTS 240

QY 241 GRCLLSLSQKRVVLGLPGLITIRCVSRGVV 268
DB 241 GRCLLSLSQKRVVLGLPGLITIRCVSRGVV 268

RESULT 2
AAB62320
ID AAB62320 standard; Protein; 272 AA.

XX AAB62320;

XX 29-JUN-2001 (first entry)

XX Rat sodium channel beta-1A subunit.

XX Sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
XX sodium channel alpha subunit; analgesic; neuroprotective.

OS Rattus sp.

XX Key Location/Qualifiers

XX MISC-difference 119

XX /note="the corresponding nucleotide sequence encodes a
XX residue Tyr at position 119, which is not indicated in
XX the present sequence"

XX W0200123570-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000MO-US27034.

XX 30-SEP-1999; 99US-0156837.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX D'Andrea M, Rogers KE;

XX WPI: 2001-281683/29.

XX N-PSDB; AAF57675.

XX Screening for sodium channel activity modulators, used to decrease
XX neuropathic pain, comprises contacting a candidate compound with a cell
XX expressing the channel.

XX Example 1; Page 120-121; 124pp; English.

XX The invention relates to a method of screening for a modulator of sodium
XX channel activity that comprises contacting a candidate modulator with a
XX cell co-expressing a sodium channel beta-1A subunit with a sodium channel
XX alpha subunit, and determining the effect of the candidate modulator on
XX the sodium channel function in the cell. The method is useful for
XX identifying sodium channel activity modulators, preferably causing
XX decreased beta 1A subunit expression. The modulators can be used to
XX decrease neuropathic pain, and to decrease the number of febrile seizures
XX in an individual. The present sequence represents a rat sodium channel
XX beta-1A subunit.

XX Sequence 272 AA;

Query Match 55.4%; Score 799.5; DB 22; Length 272;
Best Local Similarity 68.8%; Pred. No. 5.6e-73;

Matches 172; Conservative 14; Mismatches 39; Indels 25; Gaps 8;

QY 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMFTFKILICISCKRSEETAETETWTFR 60
DB 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMFTFKILICISCKRSEETAETETWTFR 60

QY 61 QKGTSEFVKILRYENEVQLLEDERFEGRVVWNGSGRTKLDLSIFITVTVYHSGDYE 120
DB 61 QKGTSEFVKILRYENEVQLLEDERFEGRVVWNGSGRTKLDLSIFITVTVYHSGDYE 120

QY 121 CHVYRLFFENYENTSVVKKIHIEVDKSGSACPTVTHRRARMDRQAVDRGTWL 180
DB 121 CHVYRLFFENYENTSVVKKIHIEVDKSGSACPTVTHRRARMDRQAVDRGTWL 180

QY 181 CAMPANRPO--QRAEGSSPCPLQMLPFLSSPRGQ--SMVPHRRSGYRTQCL--H 234
DB 181 CAMPANRPO--QRAEGSSPCPLQMLPFLSSPRGQ--SMVPHRRSGYRTQCL--H 234

QY 235 LCQMTSGRCL 244
DB 235 LCQMTSGRCL 244

QY 222 SCCVTSDCGI 231
DB 222 SCCVTSDCGI 231

RESULT 3
AAB20371
ID AAB20371 standard; Protein; 272 AA.

XX AAB20371;

DT 11-JUN-2001 (first entry)
 XX Sodium channel beta1a subunit.
 DE Sodium channel beta1a; rat; splice variant; analgesic; cardiant;
 XX pain; seizure; therapy.
 KW Rattus sp.
 OS
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..19
 XX /label= signal_peptide
 XX Protein 20..272
 XX /label= Mature_protein
 XX Domain 215..233
 XX /label= Transmembrane_domain
 XX
 XX WO200123571-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000MO-US27119.
 XX
 XX 30-SEP-1999; 99US-0156837.
 XX
 XX (UNMI) UNIV MICHIGAN.
 XX (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 XX Isom LL, Kazen-Gillespie K, Rogers KE;
 XX
 XX WPI; 2001-258136/26.
 XX N-PSDB; AAF30669.
 XX
 XX An isolated nucleic acid encoding a sodium channel beta1a subunit
 PT polypeptide, useful for identifying modulators of sodium channel beta1a
 PT subunits and treating neuropathic pain -
 XX
 PS Claim 10; Page 123-124; 121pp; English.
 XX
 XX The present sequence is that of a novel rat sodium channel beta1a
 CC subunit, which is a splice variant of sodium channel beta1, resulting
 CC from retention of intron 3 containing an in-frame stop codon. This
 CC alternative splicing event produces a novel C-terminus that includes
 CC an extracellular region, a transmembrane segment, and a short
 CC intracellular domain. Western blotting showed beta1a reactive
 CC peptides of approximately 50 kDa expressed in heart, skeletal muscle,
 CC and adrenal gland, but not in adult brain or spinal cord. Methods
 CC and compositions for using beta1a proteins and nucleic acids are
 CC described. A claimed method of screening for a modulator of sodium
 CC channel activity utilizes a cell co-expressing a sodium channel
 CC beta1a subunit and a sodium channel alpha subunit. A claimed method
 CC for decreasing neuropathic pain, and a claimed method for decreasing
 CC the number of fibrillar seizures in an individual, both involve
 CC administering a modulator of the sodium channel beta1a subunit.
 CC
 XX
 XX Sequence 272 AA:
 SQ
 Query Match 55.4%; Score 799.5; DB 22; Length 272;
 Best Local Similarity 68.8%; Pred. No. 5.6e-73;
 Matches 172; Conservative 14; Mismatches 39; Indels 25; Gaps 8;
 QY 1 MGRLLALVGAALVSSACGCVSEVDETEAVYGMFKILICISKRSETNAETFTWTFR 60
 DB 1 MGRLLALVGAALVSSACGCVSEVDETEAVYGMFKILICISKRSETNAETFTWTFR 60
 QY 61 OKGTEEFVKILRYENEVLOLEDERPEGRVWNGSGRTKLODLSIFITNTVYNSGDYE 120
 DB 61 OKGTEEFVKILRYENEVLOLEDERPEGRVWNGSGRTKLODLSIFITNTVYNSGD-E 119
 QY 121 CHVRLLEFFENYEHNTSVVKKIHIEVVDKSGSACPFVTHRIARWRDRQAVDRGML 180
 DB 120 CHVRLLEFFENYEHNTSVVKKIHIEVVDKSGMS-----LVTLMDARWRDRKGRDL--- 171

QY 181 CAMPANRPO--ORAECEGSSPCFLQWPLFLSSPRRQ-SMPVHRSGRTOLC---H 234
 DB 172 ---VSHRGQLTPRSHRGKOTPLVLETSAL---QHTGGQIRTPPTPTG---MCIGLH 221
 QY 235 LCCMTSGRCL 244
 DB 222 SCVTSDGCI 231
 RESULT 4
 AAB36031
 ID AAB36031 standard; protein: 218 AA.
 XX
 XX AAB36031;
 XX
 XX 15-FEB-2001 (first entry)
 XX
 XX Rat beta1 subunit, SEQ ID NO: 44.
 XX
 XX Rat; beta sub-unit; beta3; analgesic; anticonvulsant;
 XX cerebroprotective; vasotropic; cardiant; nootropic; cyrostatic;
 XX dermatological; gene therapy; voltage-gated sodium channel; pain;
 XX epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
 XX familial nonchromaffin paraganglioma; phenylketonuria;
 XX Charcot Marie Tooth disease; beta1.
 XX
 XX Rattus sp.
 XX
 XX WO200063367-A1.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-FEB-2000; 2000MO-EP01783.
 XX
 XX 15-APR-1999; 99US-0129473.
 XX
 XX (WARR) WARNER LAMBERT CO.
 XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 XX Cox P, Dixon A, Jackson A, Morgan K;
 XX
 XX WPI; 2000-665241/64.
 XX
 XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT sodium channel, and their corresponding polypeptides, useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PT epilepsy and stroke -
 XX
 PS Disclosure; Fig 4; 88pp; English.
 XX
 XX The present sequence is given in a specification relating to a novel
 CC family of beta sub-unit proteins from a voltage-gated sodium channel.
 CC Human and rat beta sub-units, which have been collectively identified
 CC as beta3, have been isolated. The polynucleotides and polypeptides are
 CC useful for screening for agonists and antagonists of sodium channels.
 CC The agonists, antagonists, proteins and nucleic acids may be used
 CC diagnosis of treating diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
 CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin
 CC paraganglioma, Phenylketonuria and Charcot Marie Tooth disease.
 CC
 XX
 XX Sequence 218 AA:
 SQ
 Query Match 52.0%; Score 751; DB 21; Length 218;
 Best Local Similarity 92.9%; Pred. No. 3.6e-68;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MGRLLALVGAALVSSACGCVSEVDETEAVYGMFKILICISKRSETNAETFTWTFR 60
 DB 1 MGRLLALVGAALVSSACGCVSEVDETEAVYGMFKILICISKRSETNAETFTWTFR 60
 QY 61 OKGTEEFVKILRYENEVLOLEDERPEGRVWNGSGRTKLODLSIFITNTVYNSGDYE 120

Db 61 OKGTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLSIFITNTVYHSGDYE 120
 QY 121 CHVYRLFFPENYEHTSVVKKIHLEVDKGSAA 155
 Db 121 CHVYRLFFPENYEHTSVVKKIHLEVDKANDMA 155

RESULT 5

AAB62326
 ID AAB62326 standard; Protein; 218 AA.

AC AAB62326;

DT 29-JUN-2001 (first entry)

DE Rat sodium channel beta-1 subunit amino acid sequence.

KW Sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
 KW sodium channel beta-1 subunit; analgesic; neuroprotective.

OS Rattus sp.

XX WO200123570-A2.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-US27034.

PR 30-SEP-1999; 99US-0156837.

PA (ORTH) ORTHO-MCNEIL PHARM INC.

PI D'Andrea M, Rogers KE;

DR WPI; 2001-281683/29.

PT Screening for sodium channel activity modulators, used to decrease
 PT neuropathic pain, comprises contacting a candidate compound with a cell
 PT expressing the channel -
 XX Examples; Fig 1B; 124pp; English.

CC The invention relates to a method of screening for a modulator of sodium
 CC channel activity that comprises contacting a candidate modulator with a
 CC cell co-expressing a sodium channel beta-1A subunit with a sodium channel
 CC the sodium channel function in the cell. The method is useful for
 CC identifying sodium channel activity modulators, preferably causing
 CC decreased beta 1A subunit expression. The modulators can be used to
 CC decrease neuropathic pain, and to decrease the number of febrile seizures
 CC in an individual. The present sequence represents a rat sodium channel
 CC beta-1 subunit, used in homology studies with the beta-1A subunit.

XX Sequence 218 AA;

Query Match 52.0%; Score 751; DB 22; Length 218;
 Best Local Similarity 92.9%; Pred. No. 3.6e-68;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMTFKILICISCRKRSSTTAEFTETWTFR 60
 Db 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMTFKILICISCRKRSSTTAEFTETWTFR 60
 QY 61 OKGTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLSIFITNTVYHSGDYE 120
 Db 61 OKGTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLSIFITNTVYHSGDYE 120
 QY 121 CHVYRLFFPENYEHTSVVKKIHLEVDKGSAA 155
 Db 121 CHVYRLFFPENYEHTSVVKKIHLEVDKANDMA 155

RESULT 6

AAB50260

ID AAB50260 standard; Protein; 218 AA.

XX AAB50260;

DT 13-MAR-2001 (first entry)

DE Rabbit sodium channel beta1 protein.

KW Rat; sodium channel beta3 protein; A19x94h5; pain; sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction.

OS Oryctolagus cuniculus.

PN WO200069912-A1.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US13144.

PR 14-MAY-1999; 99US-0134198.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

DR WPI; 2001-122743/13.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics -
 XX Disclosure; Fig 3; 145pp; English.

CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated A19x94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptive nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics.

XX Sequence 218 AA;

Query Match 51.9%; Score 749; DB 22; Length 218;
 Best Local Similarity 92.9%; Pred. No. 5.8e-68;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMTFKILICISCRKRSSTTAEFTETWTFR 60
 Db 1 MGRLLALVVGALVSSAGCGVEVDSETEAVYGMTFKILICISCRKRSSTTAEFTETWTFR 60
 QY 61 OKGTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLSIFITNTVYHSGDYE 120
 Db 61 OKGTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLSIFITNTVYHSGDYE 120
 QY 121 CHVYRLFFPENYEHTSVVKKIHLEVDKGSAA 155
 Db 121 CHVYRLFFPENYEHTSVVKKIHLEVDKANDMA 155

RESULT 7

ID AAB22576
 AAB22576 standard; Protein; 1176 AA.

AC AAB22576;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22567.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KM		food supplement; medical imaging;diagnostic; genetic disorder.
XX		
OS	Homo sapiens.	
XX		
PN	MO200175067-A2.	
PD	11-OCT-2001.	
XX		
PF	30-MAR-2001; 2001WO-US08631.	
XX		
PR	31-MAR-2000; 2000US-0540217.	
PR	23-AUG-2000; 2000US-0649167.	
XX		
PA	(HYSE-) HYSEQ INC.	
XI	Dzmanac RT, Liu C, Tang YT;	
DR	WPI; 2001-639362/73.	
N-PSDB; AAS86763.		
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	biodiversity -	
XX		
PS	Claim 20; SEQ ID No 52935; 103bp; English.	
CC	The invention relates to isolated polynucleotide (I) and	
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC	and gene mapping, and in recombinant production of (II). The	
CC	polynucleotides are also used in diagnostics as expressed sequence tags	
GC	for identifying expressed genes. (I) is useful in gene therapy techniques	
CC	to restore normal activity of (II) or to treat disease states involving	
CC	(II). (II) is useful for generating antibodies against it, detecting or	
CC	quantitating a polypeptide in tissue, as molecular weight markers and as	
CC	a food supplement. (II) and its binding partners are useful in medical	
CC	imaging of sites expressing (II). (I) and (II) are useful for treating	
CC	disorders involving aberrant protein expression or biological activity.	
CC	The polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG30377 represent novel human	
CC	diagnostic amino acid sequences of the invention.	
CC	Note: The sequence data for this patent did not appear in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
SQ	Sequence 1176 AA:	
	Query Match 18.2%; Score 263.5; DB 22; Length 1176;	
	Best Local Similarity 41.6%; Pred. No. 1,7e-17;	
	Matches 62; Conservative 20; Mismatches 54; Indels 13; Gaps 5	
Oy	21 CVDNSTEAVVGMFTFLICISCKRRESENAEFTEWTFPROKGEPEFVKILRYENETLOL 80	
Db	994 CVEPSTETEVNQGPMTLCRTCSCKRREVEYTVVFTRPGGGKDL-IYERNGHOEV 1052	
Oy	81 EEDRFEGRVVMNSRGTKDLDLSITITVTYNHSGDYCHVYRLLFENYEHTNSVVK 140	
Db	1053 ESP--FGRIQWNMS---KOLQDVSIIVLVNTLTNDSDGLTYCNVSRBEPEAHHPFVYKTR 1107	
Oy	141 KIHIEVVDKG--ESGAACPFTV-----TH 162	
Db	1108 LIPLRVTEEGLISSSNVPMINIELGRNTH 1136	
RESULT 8		
ID	AAB36020 standard; protein; 159 AA.	
XX		
AC	AAB36020;	

[illegible]

DT 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 1874.
 DE
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
 PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW,
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R,
 XX
 DR WPI: 2001-476283/51.
 DR N-PSDB; AAK52345.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 4260; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 CC
 XX
 SQ Sequence 195 AA;
 XX
 Query Match 17.9%; Score 258.5; DB 22; Length 195;
 Best Local Similarity 43.2%; Pred. No. 4.9e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 XX
 QY 5 LALVGAALVSSACGCVVDSETEAVVGMFKILICISCKRSEETNAETFTWTFRQKT 64
 DB 10 LASLVLIVWVSVCFPCVCEVPSETEAVQGNPMKLCISCKRSEVEATTVEMFRRPGG 69
 QY 65 EEFVKILARENEVLQLEDERFEGRVWNGSRGTDLDDLSIFITNTVYVNSGDYCHVY 124
 DB 70 KDFLITYYRNHGHVESP--FQGRLOWNGS---KDLDVSVITLVNTLNSGYTCNVS 123
 QY 125 RLFFENYEHTSVVKKIHIEVDK-GE 151
 DB 124 REFEEAHRPVPKTRRLIPRTBERGE 151

RESULT 10
 AAB36002
 ID AAB36002 standard; protein; 215 AA.
 XX
 AC AAB36002;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Human beta3 subunit.
 XX
 KW Human; beta sub-unit; beta3; analgesic; anticonvulsant;
 KW cerebroprotective; vasotropic; cardiant; nootropic; cycostatic;
 KW dermatological; gene therapy; voltage-gated sodium channel; pain;
 KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromatin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease.
 XX
 OS Homo sapiens.
 PN WO200063367-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-FEB-2000; 2000MO-EP01783.
 XX
 PR 15-APR-1999; 99US-0129473.
 XX
 PA (WARN) WARNER LAMBERT CO.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Cox P, Dixon A, Jackson A, Morgan K,
 PI
 DR WPI: 2000-665241/64.
 DR N-PSDB; AAC67837.
 XX
 PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT sodium channel, and their corresponding polypeptides, useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PT epilepsy and stroke -
 XX
 PS Claim 34; Fig 4; 88pp; English.
 XX
 CC The present sequence is given in the claims of a specification
 CC relating to a novel family of beta sub-unit proteins from a
 CC voltage-gated sodium channel. Human and rat beta sub-units, which
 CC have been collectively identified as beta3, have been isolated.
 CC The polynucleotides and polypeptides are useful for screening for
 CC agonists and antagonists of sodium channels. The agonists, antagonists,
 CC proteins and nucleic acids may be used for diagnosing of treating diseases
 CC or conditions associated with voltage-gated sodium channels, e.g. pain,
 CC epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, familial
 CC nonchromatin Paraganglioma, phenylketonuria and Charcot Marie Tooth
 CC disease.
 CC
 XX
 SQ Sequence 215 AA;
 XX
 Query Match 17.9%; Score 258.5; DB 21; Length 215;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 XX
 QY 5 LALVGAALVSSACGCVVDSETEAVVGMFKILICISCKRSEETNAETFTWTFRQKT 64
 DB 10 LASLVLIVWVSVCFPCVCEVPSETEAVQGNPMKLCISCKRSEVEATTVEMFRRPGG 69
 QY 65 EEFVKILARENEVLQLEDERFEGRVWNGSRGTDLDDLSIFITNTVYVNSGDYCHVY 124
 DB 70 KDFLITYYRNHGHVESP--FQGRLOWNGS---KDLDVSVITLVNTLNSGYTCNVS 123
 QY 125 RLFFENYEHTSVVKKIHIEVDK-GE 151
 DB 124 REFEEAHRPVPKTRRLIPRTBERGE 151

RESULT 11
 AAB85206
 ID AAB85206 standard; Protein; 215 AA.
 AC AAB85206;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human novel sodium channel beta-like subunit.
 XX
 DE Sodium channel; sensory neuron specific channel; beta-like subunit;
 KW SNS; therapeutic; pain; analgesic.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 38..122
 FT /note="immunoglobulin domain"
 FT 157..176
 FT Domain /note="transmembrane domain"
 FT
 PN WO200144293-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 14-DEC-2000; 2000MO-GB04802.
 XX
 PR 17-DEC-1999; 99GB-0029970.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI Plumpston M, Powell AJ, Sansau P;
 DR WPI; 2001-398129/42.
 DR N-PSDB; AAB84146.
 XX
 PT Novel sub-unit for voltage-gated sodium channel proteins for producing
 PT agents useful for treating pain
 XX
 PS Claim 1; Fig 2; 31pp; English.
 XX
 CC The invention provides a novel beta-like sub-unit for voltage-gated
 CC sodium ion channel polypeptide, specifically a sensory neuron specific
 CC channel (SNS) subunit. The novel beta-like subunit is useful for
 CC producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 CC present sequence represents a human novel sodium channel beta-like
 CC subunit.
 CC
 SQ Sequence 215 AA;
 XX
 SQ
 Query Match 17.9%; Score 258.5; DB 22; Length 215;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 QY 5 LALVVGALVSSACGGCEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETWTRQKGT 64
 DB 10 LASLVLITVWSVCPVCEVPESTETAVQGNPMKRCISCKREVEATVVMFYRPEGG 69
 QY 65 EEVFKILRYENEVLQLEDERFEGRVVNGSRGTRKLDLSTFIVNTVYHSGDYEGHY 124
 DB 70 KDFL-IYEYRNGHVEESP--FOGRLQWNGS---KDLQDVSTIVLVNTLNDLSGLYTCNV 123
 QY 125 RLFPENYEHTSVVKKIHIEVDK-GE 151
 DB 124 REFEFAHRFPVKTTRILPLRVTEAGE 151
 XX
 RESULT 12
 AAB05689
 ID AAB05689 standard; Protein; 215 AA.
 XX

AC AAB05689;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Human signal transduction protein clone amy2_2f18.
 XX
 DE Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KW gene therapy.
 KW
 OS Homo sapiens.
 XX
 PN WO200198454-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 25-APR-2001; 2001MO-IB02050.
 XX
 PR 25-APR-2000; 2000US-199380P.
 XX
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S;
 DR WPI; 2002-055860/07.
 DR N-PSDB; ABA93727.
 XX
 PT Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy -
 XX
 PS Claim 1; Page 176; 611pp; English.
 XX
 CC The present invention describes assemblages and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for
 CC example they may be used in profiling assays, for providing large arrays
 CC of human genetic material for implementing large-scale screening
 CC strategies and for treating diseases via gene therapy procedures.
 CC
 SQ Sequence 215 AA;
 XX
 SQ
 Query Match 17.9%; Score 258.5; DB 23; Length 215;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 QY 5 LALVVGALVSSACGGCEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETWTRQKGT 64
 DB 10 LASLVLITVWSVCPVCEVPESTETAVQGNPMKRCISCKREVEATVVMFYRPEGG 69
 QY 65 EEVFKILRYENEVLQLEDERFEGRVVNGSRGTRKLDLSTFIVNTVYHSGDYEGHY 124
 DB 70 KDFL-IYEYRNGHVEESP--FOGRLQWNGS---KDLQDVSTIVLVNTLNDLSGLYTCNV 123
 QY 125 RLFPENYEHTSVVKKIHIEVDK-GE 151
 DB 124 REFEFAHRFPVKTTRILPLRVTEAGE 151
 XX
 RESULT 13
 AAB36021
 ID AAB36021 standard; Protein; 159 AA.
 XX
 AC AAB36021;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Rat beta3 subunit peptide, SEQ ID NO: 23.
 XX
 KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant;
 XX

KW cerebroprotective; vasotropic; cardiast; nootropic; cyrostatic;
 KW dermatological; gene therapy; voltage-gated sodium channel; pain;
 KW epilepsy; stroke; ischemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease.

OS Rattus sp.

XX WO200063367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000MO-EP01783.

XX 15-APR-1999; 99US-0129473.

XX (WARN) WARNER LAMBERT CO.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

XX WPI; 2000-665241/64.

PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT sodium channel, and their corresponding polypeptides, useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PT epilepsy and stroke.

PS Claim 36; Page 76-77; 88pp; English.

CC The present sequence is given in the claims of a specification
 CC relating to a novel family of beta sub-unit proteins from a
 CC voltage-gated sodium channel. Human and rat beta sub-units, which
 CC have been collectively identified as beta3, have been isolated.
 CC The polynucleotides and polypeptides are useful for screening for
 CC agonists and antagonists of sodium channels. The agonists, antagonists,
 CC proteins and nucleic acids may be used diagnosing or treating diseases,
 CC or conditions associated with voltage-gated sodium channels, e.g. pain,
 CC epilepsy, stroke, ischemia, heart disease, Jacobsen Syndrome, Familial
 CC Nonchromaffin Paraganglioma, Phenylketonuria and Charcot Marie Tooth
 CC disease.

XX Sequence 159 AA;

Query Match 17.8%; Score 257.5; DB 21; Length 159;
 Best Local Similarity 44.7%; Pred. No. 4.7e-18;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTEFKILCISCKRSEETNAETFTWTFROKGTSEFVKILRYENEVLQ 80
 Db 26 CVEVPSSETEAVQGNPMKLRICISCKRSEETNAETFTWTFROKGTSEFVKILRYENEVLQ 80
 QY 81 EEDERFEGRVVWNGSRGTDLQDLSIFITNTVYVNHSGDCECHVRLLPFENEHNTSVK 140
 Db 85 ESP--FGRLQWNGS--KDLQDVSTIVLVNTLNDGLTYCNVSRFEFEFAHRPFVKTR 139

QY 141 KHIIEVDK-GE 151
 Db 140 LIPLRVTEAGE 151

RESULT 14
 AAB50245
 ID AAB50245 standard; Protein; 191 AA.

XX AAB50245;

XX 13-MAR-2001 (first entry)

DE Rat sodium channel beta3 protein A19x94h5 mature protein.

KW Rat; sodium channel beta3 protein; A19x94h5; pain; sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction.

XX Rattus sp.

XX WO200069912-A1.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000MO-US13144.

XX 14-MAY-1999; 99US-0134198.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2001-122743/13.

XX N-PSDB; AAC90600.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.

PS Claim 9; Fig 2; 145pp; English.

CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated A19x94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptive nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics.

XX Sequence 191 AA;

Query Match 17.8%; Score 257.5; DB 22; Length 191;
 Best Local Similarity 44.7%; Pred. No. 6e-18;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTEFKILCISCKRSEETNAETFTWTFROKGTSEFVKILRYENEVLQ 80
 Db 2 CVEVPSSETEAVQGNPMKLRICISCKRSEETNAETFTWTFROKGTSEFVKILRYENEVLQ 60

QY 81 EEDERFEGRVVWNGSRGTDLQDLSIFITNTVYVNHSGDCECHVRLLPFENEHNTSVK 140
 Db 61 ESP--FGRLQWNGS--KDLQDVSTIVLVNTLNDGLTYCNVSRFEFEFAHRPFVKTR 115

QY 141 KHIIEVDK-GE 151
 Db 116 LIPLRVTEAGE 127

RESULT 15
 AAB36001
 ID AAB36001 standard; protein; 215 AA.

XX AAB36001;

XX 15-FEB-2001 (first entry)

DE Rat beta3 subunit.

KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
 KW vasotropic; cardiast; nootropic; cyrostatic; dermatological;
 KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
 KW ischemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease.

OS Rattus sp.
 XX WO200063367-A1.

PD 26-OCT-2000.

XX 24-FEB-2000; 2000MO-EP01783.

XX 15-APR-1999; 99US-0129473.

XX (WARN) WARNER LAMBERT CO.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

PI WPI; 2000-665241/64.

XX N-PSDB; AAC67836.

DR Novel nucleic acids encoding a beta-3 subunit from a voltage-gated

PT sodium channel, and their corresponding polypeptides, useful for

PT detecting and treating sodium channel-associated conditions, e.g. pain,

PT epilepsy and stroke -

PS Claim 33; Fig 4; 88pp; English.

XX The present sequence is given in the claims of a specification

CC relating to a novel family of beta sub-unit proteins from a

CC voltage-gated sodium channel. Human and rat beta sub-units, which

CC have been collectively identified as beta3, have been isolated

CC The polynucleotides and polypeptides are useful for screening for

CC agonists and antagonists of sodium channels. The agonists, antagonists,

CC proteins and nucleic acids may be used diagnosing of treating diseases

CC or conditions associated with voltage-gated sodium channels, e.g. pain,

CC epilepsy, stroke, ischemia, heart disease, Jacobsen Syndrome, Familial

CC Nonchromatin Paraganglioma, Phenylketonuria and Charcot Marie Tooth

CC disease.

SQ Sequence 215 AA;

Query Match 17.8%; Score 257.5; DB 21; Length 215;

Best Local Similarity 44.7%; Pred No. 7e-18; Mismatches 47; Indels 7; Gaps 4;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

OY 21 CVEVDSETEAVVGMTPFKILICISCKRSEETNAETFTWTFROKTEBPFVKILAYENEVLQ 80

DB 26 CVEVPSETEAVVGMTPFKILICISCKRSEETNAETFTWTFROKTEBPFVKILAYENEVLQ 84

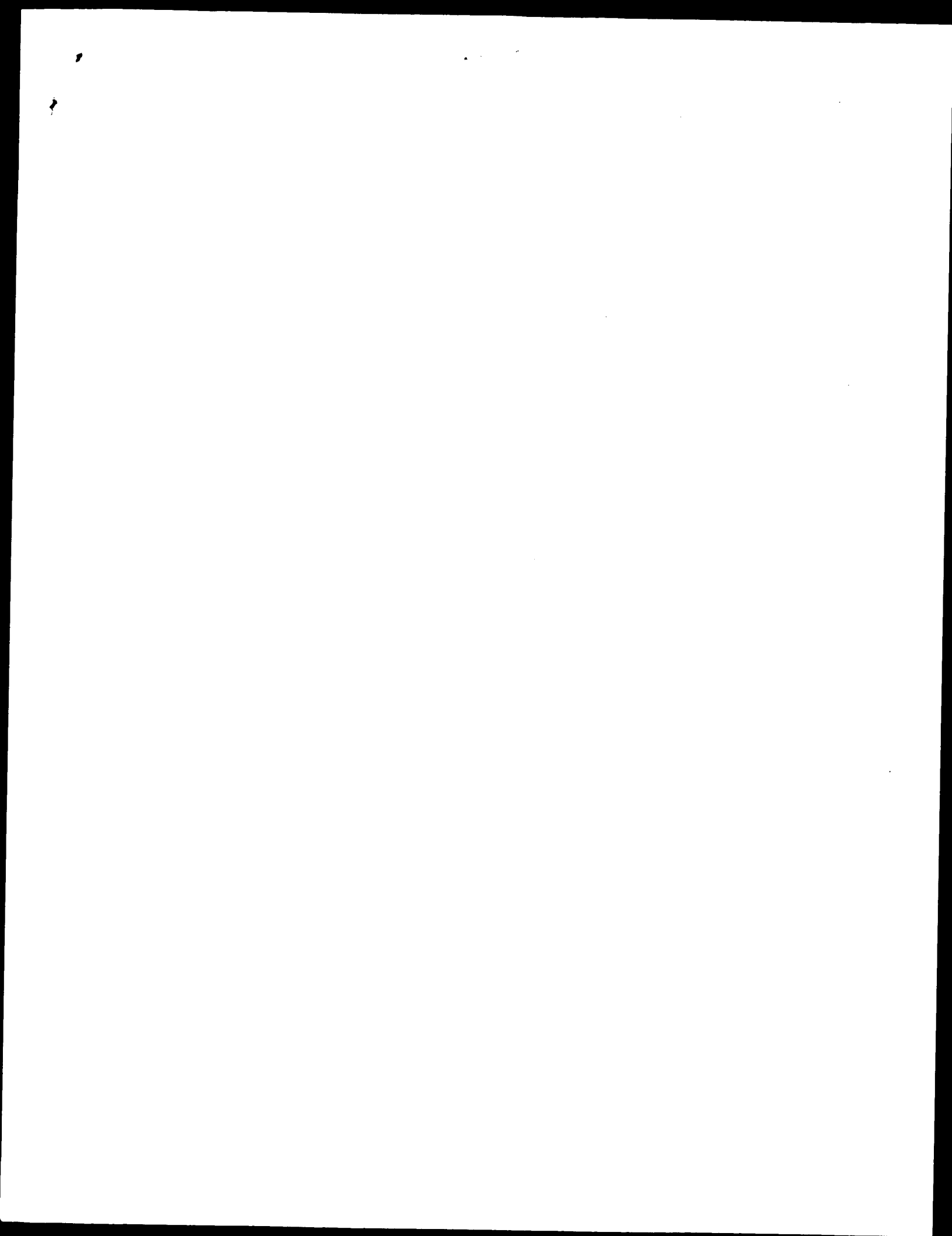
OY 81 EEDERFEGRVVNGSKCTDLODLSIFITNVYVNHSGDYCHVYRLFPENYEHTSVK 140

DB 85 ESP--FQGRLOMNGS--KLDQVSTIVLVNLTNDGLTTCNVSRFEFEARFPVKTR 139

OY 141 KIHIEVVDK-GE 151

DB 140 LIPLRVTEPAGE 151

Search completed: January 29, 2003, 13:28:15
Job time : 38 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:27:37 ; Search time 15 Seconds
(without alignments)
525.690 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444
Sequence: 1 MGRLLALVVGALVSSACGG.....QRVLGLGIIIRCVSRGV 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115.5	8.0	209	US-09-430-503-20	Sequence 20, Appl
2	115.5	8.0	209	US-09-430-503-24	Sequence 24, Appl
3	115.5	8.0	269	US-09-430-503-4	Sequence 4, Appl
4	115.5	8.0	269	US-09-430-503-6	Sequence 6, Appl
5	115.5	8.0	269	US-09-430-503-8	Sequence 8, Appl
6	114.5	7.9	159	US-09-430-503-34	Sequence 34, Appl
7	114.5	7.9	159	US-09-430-503-38	Sequence 38, Appl
8	114.5	7.9	199	US-09-430-503-42	Sequence 42, Appl
9	114.5	7.9	199	US-09-430-503-46	Sequence 46, Appl
10	114.5	7.9	209	US-09-430-503-18	Sequence 18, Appl
11	114.5	7.9	209	US-09-430-503-32	Sequence 22, Appl
12	114.5	7.9	269	US-09-430-503-2	Sequence 2, Appl
13	114.5	7.8	159	US-09-430-503-36	Sequence 36, Appl
14	112.5	7.8	159	US-09-430-503-40	Sequence 40, Appl
15	112.5	7.8	199	US-09-430-503-44	Sequence 44, Appl
16	112.5	7.8	199	US-09-430-503-48	Sequence 48, Appl
17	107.5	7.4	270	US-09-430-503-26	Sequence 26, Appl
18	107.5	7.4	270	US-09-430-503-28	Sequence 28, Appl
19	107.5	7.4	270	US-09-430-503-30	Sequence 30, Appl
20	107.5	7.4	270	US-09-430-503-32	Sequence 32, Appl
21	98	6.8	380	US-08-459-953A-9	Sequence 9, Appl
22	94	6.5	358	US-08-176-620A-12	Sequence 12, Appl
23	94	6.5	358	US-08-461-985-12	Sequence 12, Appl
24	94	6.5	358	US-09-457-040B-4	Sequence 4, Appl
25	94	6.5	360	US-09-457-040B-3	Sequence 3, Appl
26	94	6.5	364	US-09-457-040B-34	Sequence 34, Appl
27	94	6.5	415	US-08-176-620A-4	Sequence 4, Appl

28	94	6.5	415	1	US-08-463-862-4	Sequence 4, Appl
29	94	6.5	415	2	US-08-461-985-4	Sequence 4, Appl
30	94	6.5	415	2	US-08-458-887-4	Sequence 4, Appl
31	94	6.5	415	4	US-08-932-787B-4	Sequence 4, Appl
32	94	6.5	415	4	US-08-932-012C-4	Sequence 4, Appl
33	94	6.5	415	4	US-08-888-818C-4	Sequence 4, Appl
34	91.5	6.3	4302	4	US-09-052-469-6	Sequence 6, Appl
35	91.5	6.3	4302	4	US-09-052-469-6	Sequence 6, Appl
36	90.5	6.3	4302	2	US-08-658-136-5	Sequence 5, Appl
37	90.5	6.3	4302	2	US-08-460-751-2	Sequence 2, Appl
38	89	6.2	365	4	US-09-457-040B-35	Sequence 35, Appl
39	87.5	6.1	581	2	US-08-724-394A-3	Sequence 3, Appl
40	85	5.9	360	3	US-08-622-277A-14	Sequence 14, Appl
41	80.5	5.6	201	3	US-09-015-734-12	Sequence 12, Appl
42	80.5	5.6	236	3	US-09-015-734-7	Sequence 7, Appl
43	80.5	5.6	255	3	US-09-015-734-2	Sequence 2, Appl
44	80.5	5.6	581	2	US-08-724-394A-2	Sequence 2, Appl
45	80	5.5	360	4	US-09-025-580-2	Sequence 2, Appl

ALIGNMENTS

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US-09-430-503-20
; Sequence 20, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-20
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Query Match 8.0%; Score 115.5; DB 4; Length 209;
Best Local Similarity 30.6%; Pred. No. 0.00019;
Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;

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QY 3 RLALVVGAL-VSSACGGCVENDESE--AVYGMFKLICGKRRSEETMAETFEWTF 59
DB 18 RLWSVLAALGILTAGVSALEVTPKEIVANGTCKLTC-KFKSTTGGUTSVSMST 76
QY 60 ROKGTEEFVKILRYENEVLQLEDEDEREGRVWNGSRGTDLQDLSIFITVTYHSGDY 119
DB 77 QPEGADTVSFFHSQGGVYLGNTPPFKRLSW---AGDDKKDASININMQFIHNGTV 133
QY 120 ECHV 123
DB 134 ICDV 137
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RESULT 2
US-09-430-503-24
; Sequence 24, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-24

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Query Match	8.0%;	Score 115.5;	DB 4;	Length 209;
Best Local Similarity	30.6%;	Pred. No. 0.00019;		
Matches 38;	Conservative 17;	Mismatches 62;	Indels 7;	Gaps 4

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09      3 RLIALVGAAL-VSSACGGVEVDEBTE--AVYGMTPKILCISCKRSEINAETFEWTF 59
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Db      18 RMLMSTLAALGILTAGVSALEVTPKEIFVANGTQGLTC-KRKSTTGGTSSWSF 76

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60 RQKGEFVKILRYENEVLTQEEDERFERVRVWNRSGTDLQDLSFITNTVTYHSGDY 119
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77 QPEGADTVSEFFHYSGQGVLYLGNPPFECDRISW---AGDLDKKDASINIENNQFIHNQTY 133

QY	120	ECHV	123
Db	134	ICDV	137

RESULT 3
US-09-430-503-4

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1  APPLICANT: Zhao, Zhizhuang
2  TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
3  TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
4  FILE REFERENCE: Alcotney Docket No. 6355786 1242-11/2
5  CURRENT APPLICATION NUMBER: US/09/430,503
6  CURRENT FILING DATE: 1999-10-29
7  NUMBER OF SEQ. ID NOS.: 49
8  SOFTWARE: PatentIn Ver. 2.0
9  SEQ ID NO 4
10 LENGTH: 269
11 TYPE: PRT
12 ORGANISM: Homo sapiens
13 US-09-430-503-4

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Query Match	8.0%;	Score 115.5;	DB 4;	Length 269;
Best Local Similarity	30.6%;	Pred. No. 0.00027;		
Matches 38;	Conservative 17;	Mismatches 62;	Indels 7;	Gaps 4

QY 3 RLALVGAAL-VSSACGGCEVEVDSETE--AVGYMTFKLICISCKRRSETNAETFTWTF 59
 | : ||| : : | : | : | : | : | : | : |
Db 18 RWLMSVLAAALGILTAGVSALAEVTTPKEIFVANGTQGLTC-KFKSTSTTGGLTSVSMSP 76

QY 60 RQKQTEEFVKILRYENEVLQLLEDERFERFVRVWNGSRGTKLQDLSTFTNTVTYNHSGDY 11
 : : | : : : : : : : : : : : :
 Db 77 QPEGADTVTSFFHYSGQGVLYLGNYPPEFKDRISW--AGDLDKKDASINLENMGIHNHTGY 13

Qy	120	ECHV	123
Db	134	ICDV	137

RESULT 4
US-09-430-503-6
; Sequence 6, Application US/09430503
; Patent No. 6355786

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1  APPLICANT:Zhao, Zhi-zhuang
2  TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
3  TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
4  FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
5  CURRENT APPLICATION NUMBER: US/09/430,503
6  CURRENT FILING DATE: 1999-10-29
7  NUMBER OF SEQ ID NOS: 49
8  SOFTWARE: PatentIn Ver. 2.0
9  SEQ ID NO 6
10 LENGTH: 269

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-6

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Query Match	8.0%	Score 115.5;	DB 4;	Length 269;
Best Local Similarity	30.6%;	Pred. No. 0.00027;		
Matches 38;	Conservative 17;	Mismatches 62;	Indels 7;	Gaps 4;

QY 3 RLLALVGAAL-VSSAGCGCEVDSETE--AVYGMTFKILICISCKRSETNAEFTETWTF 59
 | | : ||| : : ||| : : | | : | : | :
Db 18 RLWMSVLAAALGILTGVSALEVTTPKEIFVANGTQGKLTG-KFKSTTGGLTSVSWSF 76

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Qy 60 RQGTETEEFKILRYENEVLQLEDEDEKRGVYVWNGSRGKDLQQLSIFINVTYHNSGDY 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 QREGADTVTSFHHISGGVYLGNYPPFFKDRISW--AGDLDDKXASININEMQFIHNGTY 133

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QY	120	ECHV	123
Db	134	ICDV	137

RESULT 5
US-09-430-503-8
; Sequence 8, Application US/09430503
; Patent No. 6,557,705

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? APPLICANT Zhao, Zhizhuang
? TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
? TITLE OF INVENTION: THRAEAUTIC AND SCREENING METHODS USING SAME
? FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
? CURRENT APPLICATION NUMBER: US/09/430.503
? CURRENT FILING DATE: 1999-10-29
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: Patentl In Ver. 2.0
? SEQ ID NO 8
? LENGTH: 269
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-430-503-8

```

Query Match	8.0%;	Score 115.5;	DB 4;	Length 269;
Best Local Similarity	30.6%;	Pred. No. 0.00027;		
Matches 38;	Conservative 17;	Mismatches 62;	Indels 7;	Gaps 4

QY 3 RLALVGAAL-VSSACGGCEVDSEIE--AVYGMTFKLICISCKKRSETNAEFTETWTF 59
| | | | | : : : | | | : : : |
Db 18 RRLMSVTLAALGILTAGVSALEVYTPKEIFVANGTQGKLT-C-KFKSTSTTGILTSVSNMF 76

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QY      60 RQKGTSEVVKILRYENEVLQLLEDERFEGRVVNGSKTKDLQDLSIFITNVTVNHSGDY 119
       : : | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
Db     77 QPEGADTIVSFPHYSQGQVYLGNYPFKDRISW--AGDLLDKDA SINIENMQFIHNGTY 133
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Qy	120	ECHV	123
Db	134	ICDV	137

RESULT 6
US-09-430-503-34
; Sequence 34, Application US/09430503
Default wa 00000

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1  APPLICANT: Zhao, Zhizhuang
2  TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
3  TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
4  FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
5  CURRENT APPLICATION NUMBER: US/09/430,503
6  CURRENT FILING DATE: 1999-10-29
7  NUMBER OF SEQ. ID NOS: 49
8  SOFTWARE: PatentIn Ver. 2.10
9  SEQ. ID NO 34
10 LENGTH: 159
11 TYPE: PRT

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Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.00024;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLALVGAALVSSACG-GCVDSETE--AVYGMTFKLICISCKRSENAETFEWTF 59
 DB 18 RMLWSVLAALGLTLAGVSALEVTPEKEIFVANGTGKLT-C-KFKSTSTTGGLTSVSWSF 76
 QY 60 ROKGTEEFVKILRYENEVLQLEDERFERGVRVWNGSRGTQDLODISFITNTVYVNHSGDY 119
 DB 77 QPBGADTTVSFFHYSGQGVYLGNYPPFKDRISW---AGDLDDKDKASINIENMQFIHNGTY 133
 QY 120 ECHV 123
 DB 134 ICDV 137

RESULT 11

US-09-430-503-22
 ; Sequence 22, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 22
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-430-503-22

Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.00024;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLALVGAALVSSACG-GCVDSETE--AVYGMTFKLICISCKRSENAETFEWTF 59
 DB 18 RMLWSVLAALGLTLAGVSALEVTPEKEIFVANGTGKLT-C-KFKSTSTTGGLTSVSWSF 76
 QY 60 ROKGTEEFVKILRYENEVLQLEDERFERGVRVWNGSRGTQDLODISFITNTVYVNHSGDY 119
 DB 77 QPBGADTTVSFFHYSGQGVYLGNYPPFKDRISW---AGDLDDKDKASINIENMQFIHNGTY 133
 QY 120 ECHV 123
 DB 134 ICDV 137

RESULT 12

US-09-430-503-2
 ; Sequence 2, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 2
 ; LENGTH: 269
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 US-09-430-503-2

Query Match 7.9%; Score 114.5; DB 4; Length 269;
 Best Local Similarity 30.6%; Pred. No. 0.00035;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLALVGAALVSSACG-GCVDSETE--AVYGMTFKLICISCKRSENAETFEWTF 59
 DB 18 RMLWSVLAALGLTLAGVSALEVTPEKEIFVANGTGKLT-C-KFKSTSTTGGLTSVSWSF 76
 QY 60 ROKGTEEFVKILRYENEVLQLEDERFERGVRVWNGSRGTQDLODISFITNTVYVNHSGDY 119
 DB 77 QPBGADTTVSFFHYSGQGVYLGNYPPFKDRISW---AGDLDDKDKASINIENMQFIHNGTY 133
 QY 120 ECHV 123
 DB 134 ICDV 137

RESULT 13

US-09-430-503-36
 ; Sequence 36, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 36
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-430-503-36

Query Match 7.8%; Score 112.5; DB 4; Length 159;
 Best Local Similarity 29.8%; Pred. No. 0.00027;
 Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLALVGAALVSSACG-GCVDSETE--AVYGMTFKLICISCKRSENAETFEWTF 59
 DB 18 RMLWSVLAALGLTLAGVSALEVTPEKEIFVANGTGKLT-C-KFKSTSTTGGLTSVSWSF 76
 QY 60 ROKGTEEFVKILRYENEVLQLEDERFERGVRVWNGSRGTQDLODISFITNTVYVNHSGDY 119
 DB 77 QPBGADTTVSFFHYSGQGVYLGNYPPFKDRISW---AGDLDDKDKASINIENMQFIHNGTY 133
 QY 120 ECHV 123
 DB 134 ICDV 137

RESULT 14

US-09-430-503-40
 ; Sequence 40, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:

; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 40
 ; LENGTH: 159
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 US-09-430-503-40

Query Match 7.8%; Score 112.5; DB 4; Length 159;

Best Local Similarity 29.8%; Pred. No. 0.00027;
Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4.

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Db 18 RMLWSVLAALIGLLTAGVSALEVYTPKEIFVANGTQGLTC-KFKSTSTTGGLTISVSMF 76

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Db 77 QPEGADTVTSFFHHYSGGVYLGNYPPFKDRISW---AGDLDDKDAEININEMQFIHNGTY 133

QY	120	ECHV	123
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Db 134 ICDV 137

RESULT 15

US-09-430-503-44

; Sequence 44, Application US/09430503

Patent No. 6355786

GENERAL INFORMATION:

APPLICANT: Zhao, Zhizhuang

APPLICANT: ZHAO, ZHIZHANG
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND

TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS

FILE REFERENCE: Attorney Docket No. 63557
CURRENT APPLICATION NUMBER: IIS/09/430.503

CURRENT APPLICATION NUMBER

CURRENT FILING DATE: 1999-1

NUMBER OF S

SOFTWARE: PatentIn Ver. 2.0

; SOFTWARE: E
; SEQ ID NO 44

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; SEQ ID NO 44
;
; LENGTH: 199

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; LENGTH: 199
; TYPE: PRT

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ORGANISM: Homo sapiens
US-09-430-503-44

Query Match 7.8%; Score 112.5; DB 4; length 199;

Best Local Similarity 29.8%; Pred. No. 0.00037;
Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4

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18 PWWSVYAAAGILTAGVSALEYTPKEIFVANGTQGIYC-KERKSTITGGILTSVSMF 76

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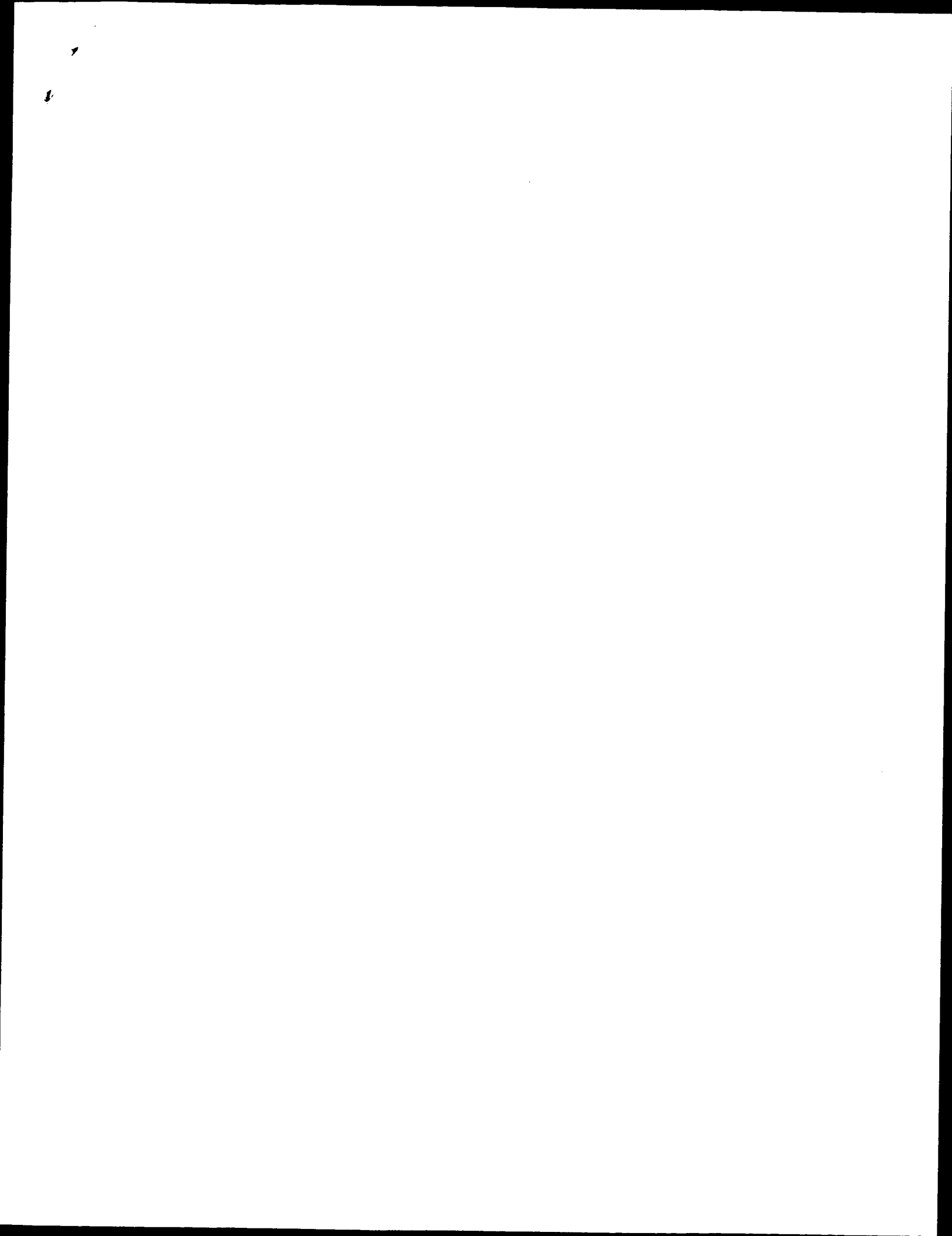
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98	191	TCNY	198
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Search completed: January 29, 2003, 13:29:59

Job time : 16 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:28:37 ; Search time 13 Seconds
(without alignments)
415.989 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444
Sequence: 1 MGRLLALVVGALVSSACGG.....QRVVLGILGIIIRCVSRGV 268

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB pep.*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB pep.*
4: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444	100.0	268	10	US-09-875-456A-14
2	751	52.0	218	10	US-09-997-579-44
3	749	51.9	218	9	US-10-028-191-20
4	258.5	17.9	159	10	US-09-997-579-22
5	258.5	17.9	215	10	US-09-997-579-2
6	257.5	17.8	191	10	US-09-997-579-23
7	257.5	17.8	191	9	US-10-028-191-4
8	257.5	17.8	215	9	US-10-028-191-1
9	257.5	17.8	215	10	US-09-997-579-1
10	251	17.4	111	9	US-10-028-191-5
11	114.5	7.9	269	9	US-10-028-072-530
12	110.5	7.7	215	9	US-09-992-558-389
13	110.5	7.7	215	9	US-09-989-253A-389
14	110.5	7.7	215	9	US-09-989-735-389
15	110.5	7.7	215	9	US-09-990-444-389
16	110.5	7.7	215	9	US-09-989-730-389
17	110.5	7.7	215	9	US-09-990-436-389
18	110.5	7.7	215	9	US-09-991-181-389
19	110.5	7.7	215	9	US-09-993-687-389

20	110.5	7.7	215	9	US-09-989-734-389	Sequence 389, App
21	110.5	7.7	215	9	US-10-028-072-488	Sequence 488, App
22	110.5	7.7	215	9	US-09-997-653-389	Sequence 389, App
23	110.5	7.7	215	10	US-09-989-722-389	Sequence 389, App
24	110.5	7.7	215	10	US-09-989-723-389	Sequence 389, App
25	110.5	7.7	215	10	US-09-989-279-389	Sequence 389, App
26	110.5	7.7	215	10	US-09-989-727-389	Sequence 389, App
27	110.5	7.7	215	10	US-09-989-732-389	Sequence 389, App
28	110.5	7.7	215	10	US-09-991-073-389	Sequence 389, App
29	110.5	7.7	215	10	US-09-990-442-389	Sequence 389, App
30	110.5	7.7	215	10	US-09-991-163-389	Sequence 389, App
31	110.5	7.7	215	10	US-09-993-604-389	Sequence 389, App
32	110.5	7.7	215	10	US-09-990-456-389	Sequence 389, App
33	110.5	7.7	215	10	US-09-989-721-389	Sequence 389, App
34	110.5	7.7	215	10	US-09-990-968A-2	Sequence 45, App1
35	90.5	6.3	4303	9	US-09-997-579-45	Sequence 12, App1
36	90	6.2	119	10	US-10-053-107-12	Sequence 6, App1
37	89.5	6.2	235	9	US-09-959-845-6	Sequence 4, App1
38	89.5	6.2	438	9	US-09-959-845-4	Sequence 16, App1
39	89.5	6.2	510	9	US-09-896-738-16	Sequence 11, App1
40	89.5	6.2	549	9	US-09-910-174A-11	Sequence 10, App1
41	87.5	6.1	523	10	US-09-953-864-10	Sequence 1159, App
42	87.5	6.1	523	10	US-09-764-864-1159	Sequence 15, App1
43	87.5	6.1	235	10	US-09-896-738-15	
44	82	5.7	276	9		
45	80.5	5.6				

ALIGNMENTS

RESULT 1
US-09-875-456A-14
Sequence 14, Application US/09875456A
Patent No. US20020045229A1
GENERAL INFORMATION:
APPLICANT: Qim, Ning
APPLICANT: Codd, Ellen
APPLICANT: D'Andrea, Michael
TITLE OF INVENTION: DNA encoding human beta1a sodium channel subunit
FILE REFERENCE: OPT-1221
CURRENT APPLICATION NUMBER: US/09/875, 456A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-456A-14

Query Match	100.0%	Score 1444	DB 10	Length 268
Best Local Similarity	100.0%	Pred. No. 2	1e-127	
Matches 268	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MGRLLALVVGALVSSACGGCCEVDSETEAVYGMFTPIILICSCRRSEETAETFTETFR	60	
DB	1	MGRLLALVVGALVSSACGGCCEVDSETEAVYGMFTPIILICSCRRSEETAETFTETFR	60	
QY	61	QKGTSEPKILRYENEVQLLEDERFEGRVVWNSRGTKLQDLSIFITVTVNHSQDY	120	
DB	61	QKGTSEPKILRYENEVQLLEDERFEGRVVWNSRGTKLQDLSIFITVTVNHSQDY	120	
QY	121	CHVYLLFFENYEHNTSVYKKIHIEVDKSGSACPEFTVTHRAARDRWQAVDRGTWL	180	
DB	121	CHVYLLFFENYEHNTSVYKKIHIEVDKSGSACPEFTVTHRAARDRWQAVDRGTWL	180	
QY	181	CAMPANRPOARAGGSSPSCPLQMPFLSSPRGSMVPVPHRSSGYRQLCHLCMTS	240	
DB	181	CAMPANRPOARAGGSSPSCPLQMPFLSSPRGSMVPVPHRSSGYRQLCHLCMTS	240	
QY	241	GRCLLSISRVVLGPGIIRCVSRGV	268	

Db 241 GRCLLSQRVVLGPGIIRCVSRGVV 268

RESULT 2

US-09-997-579-44
 ; Sequence 44, Application US/09997579
 ; Patent No. US20020113203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge University Technical Services
 ; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
 ; TITLE OF INVENTION: channel
 ; FILE REFERENCE: 674558-2001
 ; CURRENT APPLICATION NUMBER: US/09/997,579
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: PCT/EP00/01783
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60,129,473
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Rat
 US-09-997-579-44

Query Match

Best Local Similarity 52.0%; Score 751; DB 10; Length 218;
 Best Local Similarity 92.9%; Pred. No. 7,9e-63;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRLIALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 60
 Db 1 MGRLIALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 60
 Qy 61 OKGTEEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 120
 Db 61 OKGTEEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 120
 Qy 121 CHVYRLFFENYEHTSVVKKIHIEVVDKESGAA 155
 Db 121 CHVYRLFFENYEHTSVVKKIHIEVVDKESGAA 155

RESULT 3

US-10-029-191-20
 ; Sequence 20, Application US/10029191
 ; Patent No. US20020160453A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTIS, ROY A. J.
 ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 ; FILE REFERENCE: 210147.00XX/501
 ; CURRENT APPLICATION NUMBER: US/10/029,191
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 09/569,978
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: US 60/134,198
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Legum Sp.
 US-10-029-191-20

Query Match

Best Local Similarity 51.9%; Score 749; DB 9; Length 218;
 Best Local Similarity 92.9%; Pred. No. 1.2e-62;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRLIALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 60
 Db 1 MGRLIALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 60

Db 1 MGRLIALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 60

Qy 61 OKGTEEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 120
 Db 61 OKGTEEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 120

Qy 121 CHVYRLFFENYEHTSVVKKIHIEVVDKESGAA 155
 Db 121 CHVYRLFFENYEHTSVVKKIHIEVVDKESGAA 155

RESULT 4

US-09-997-579-22
 ; Sequence 22, Application US/09997579
 ; Patent No. US20020113203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge University Technical Services
 ; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
 ; TITLE OF INVENTION: channel
 ; FILE REFERENCE: 674558-2001
 ; CURRENT APPLICATION NUMBER: US/09/997,579
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: PCT/EP00/01783
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60,129,473
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-997-579-22

Query Match

Best Local Similarity 17.9%; Score 258.5; DB 10; Length 159;
 Best Local Similarity 43.2%; Pred. No. 4.9e-17;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 5 LALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 64
 Db 5 LALVGAALVSSACGCVVEVDETEAVYGMTEFKILICISCKRRSETNAETFTWTF 64
 Qy 65 EEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 124
 Db 65 EEFVKILRYENEVQLQEDERFEGRYVNGSRGTDLQDLSIFITVYVNHSGDYE 124
 Qy 125 RLFFENYEHTSVVKKIHIEVVDKESGAA 151
 Db 125 RLFFENYEHTSVVKKIHIEVVDKESGAA 151

RESULT 5

US-09-997-579-2
 ; Sequence 2, Application US/09997579
 ; Patent No. US20020113203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge University Technical Services
 ; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
 ; TITLE OF INVENTION: channel
 ; FILE REFERENCE: 674558-2001
 ; CURRENT APPLICATION NUMBER: US/09/997,579
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: PCT/EP00/01783
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60,129,473
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 215
 ; TYPE: PRT

ORGANISM: Homo sapiens
US-09-997-579-2

Query Match 17.8%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 5 LALVYGAALYSACGGVEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETFRQKTEHFVKILRYENEVLQ 64
DB 10 LASLVLVWVSVCPVCEVPESTEAVQGNPMKLRCSCKREVEATTVEMFPRGKDFL-ITYEYRNHQEV 69
QY 65 EEFVKILRYENEVLQLEDEDFEGRVVWNGSRGTQDLSIFITNTYNSGDYECVY 124
DB 70 KDFL-ITYEYRNHQEVESP--FQGRLOMNGS---KDLQDVSIYLVNTLNDSGLYTCNV 123
QY 125 RLFFENYEHTSVYKKIHIEVDK-GE 151
DB 124 REFEFAHRPFVKTRRLIPLRVTEAGE 151

RESULT 6
US-09-997-579-23

Sequence 23, Application US/09997579
Patent No. US20020113203A1

GENERAL INFORMATION:

APPLICANT: Cambridge University Technical Services

TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

TITLE OF INVENTION: channel

TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t

FILE REFERENCE: 674558-2001

CURRENT APPLICATION NUMBER: US/09/997,579

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: PCT/EP00/01783

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60,129,473

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 159

TYPE: PRT

ORGANISM: Rat

US-09-997-579-23

Query Match

Best Local Similarity 17.8%; Score 257.5; DB 10; Length 159;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETFRQKTEHFVKILRYENEVLQ 80
DB 26 CVEVDSETEAVQGNPMKLRCSCKREVEATTVEMFPRGKDFL-ITYEYRNHQEV 84
QY 81 EEDERFEGRVVWNGSRGTQDLSIFITNTYNSGDYECVYRLFFENYEHTSVYK 140
DB 85 ESP--FQGRLOMNGS---KDLQDVSIYLVNTLNDSGLYTCNVSRFEFAHRPFVKTR 139
QY 141 KIHIEVDK-GE 151
DB 140 LIPLRVTEAGE 151

RESULT 7
US-10-029-191-4

Sequence 4, Application US/10029191

Patent No. US20020160453A1

GENERAL INFORMATION:

APPLICANT: CURTIS, RORY A. J.

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

FILE REFERENCE: 210147.00XX/5U1

CURRENT APPLICATION NUMBER: US/10/029,191

CURRENT FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 09/569,978

PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/134,198

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 191

TYPE: PRT

ORGANISM: Rattus sp.

US-10-029-191-4

Query Match

Best Local Similarity 17.8%; Score 257.5; DB 9; Length 191;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETFRQKTEHFVKILRYENEVLQ 80
DB 2 CVEVDSETEAVQGNPMKLRCSCKREVEATTVEMFPRGKDFL-ITYEYRNHQEV 60
QY 81 EEDERFEGRVVWNGSRGTQDLSIFITNTYNSGDYECVYRLFFENYEHTSVYK 140
DB 61 ESP--FQGRLOMNGS---KDLQDVSIYLVNTLNDSGLYTCNVSRFEFAHRPFVKTR 115
QY 141 KIHIEVDK-GE 151
DB 116 LIPLRVTEAGE 127

RESULT 8
US-10-029-191-2

Sequence 2, Application US/10029191

Patent No. US20020160453A1

GENERAL INFORMATION:

APPLICANT: CURTIS, RORY A. J.

TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

TITLE OF INVENTION: PROTEIN

FILE REFERENCE: 210147.00XX/5U1

CURRENT APPLICATION NUMBER: US/10/029,191

CURRENT FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 09/569,978

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/134,198

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 215

TYPE: PRT

ORGANISM: Rattus sp.

US-10-029-191-2

Query Match

Best Local Similarity 17.8%; Score 257.5; DB 9; Length 215;

Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTEFKILICISCKRSEETNAETFTETFRQKTEHFVKILRYENEVLQ 80
DB 26 CVEVDSETEAVQGNPMKLRCSCKREVEATTVEMFPRGKDFL-ITYEYRNHQEV 84
QY 81 EEDERFEGRVVWNGSRGTQDLSIFITNTYNSGDYECVYRLFFENYEHTSVYK 140
DB 85 ESP--FQGRLOMNGS---KDLQDVSIYLVNTLNDSGLYTCNVSRFEFAHRPFVKTR 139
QY 141 KIHIEVDK-GE 151
DB 140 LIPLRVTEAGE 151

RESULT 9
US-09-997-579-1

Sequence 1, Application US/09997579

Patent No. US20020113203A1

GENERAL INFORMATION:

```

; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/997,579
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRF
; ORGANISM: Rat
US-09-997-579-1

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Query Match 17.8%; Score 257.5; DB 10; Length 215;
Best Local Similarity 44.7%; Pred. No. 9e-17;
Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

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QY 21 CVEVDSETEAVYGMFKILCSKRSEINAETFTETFRQKGTBEFVKILRYENEVLQ 80
DB 26 CVEVSETEAVQGNPMKLRCSCKREVEATVVEWFYREGGKDFL-IYEYENGHOEV 84
QY 81 EEDERFEGRVVNGSRGTQDQDLSIFITVNTYNSGSDYEGYCHYRLFFENYHNISVVK 140
DB 85 ESP--FQGRLOWNGS---KDLQDVSTIVLVNTLNDGLTYCNVSRERFEFAHRPFVKTTR 139
QY 141 KIHIEVDK-GE 151
DB 140 LIPLRVTEAGE 151

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```

RESULT 10
US-10-029-191-5
; Sequence 5, Application US/10029191
; Patent No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00X/501
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRF
; ORGANISM: Rattus sp.
US-10-029-191-5

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```

Query Match 17.4%; Score 251; DB 9; Length 111;
Best Local Similarity 50.0%; Pred. No. 1.5e-16;
Matches 55; Conservative 14; Mismatches 35; Indels 6; Gaps 3;

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```

QY 21 CVEVDSETEAVYGMFKILCSKRSEINAETFTETFRQKGTBEFVKILRYENEVLQ 80
DB 2 CVEVSETEAVQGNPMKLRCSCKREVEATVVEWFYREGGKDFL-IYEYENGHOEV 60
QY 81 EEDERFEGRVVNGSRGTQDQDLSIFITVNTYNSGSDYEGYCHYRLFFENYHNISVVK 140
DB 61 ESP--FQGRLOWNGS---KDLQDVSTIVLVNTLNDGLTYCNVSRERFEFAHRPFVKTTR 105

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RESULT 11

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US-10-028-072-530
; Sequence 530, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29

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PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637

PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 7.9%; Score 114.5; DB 9; Length 269;
Best Local Similarity 30.6%; Pred. No. 0.0027;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLALVGAALVSSACG-GCDEVDSSE--AVYGMTFKILICSRARSETNAETFTWTF 59
DB 18 RLWLVLAALGLTLAGVSALEVTYKPKILFVANGTGKLTG-KPKSTSTTGGLTGSVSKSF 76
QY 60 ROKGTBEFYKILRYENEVQLAEEDERFGRVYVWNGSRCTKQLQDLSTFTVTVYTHSGDY 119
DB 77 QEGADTTVSFPHYSQGGVYLVGNVPPFDRIW--AGDLDKQASINIEHMFHNGTY 133
QY 120 ECHV 123
DB 134 TCDV 137

RESULT 12
US-09-992-598-389
Sequence 389. Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bockstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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APPLICANT: Botsstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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TITLE OF INVENTION: Acids Encoding the Same
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27     APPLICANT: Williams, P. Mickey
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29     APPLICANT: Zhang, Zemin
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55	PRIOR FILING DATE: 1998-07-01
56	PRIOR APPLICATION NUMBER: 60/091478
57	PRIOR FILING DATE: 1998-07-02
58	PRIOR APPLICATION NUMBER: 60/091544
59	PRIOR FILING DATE: 1998-07-01
60	PRIOR APPLICATION NUMBER: 60/091519
61	PRIOR FILING DATE: 1998-07-02
62	PRIOR APPLICATION NUMBER: 60/091626
63	PRIOR FILING DATE: 1998-07-02
64	PRIOR APPLICATION NUMBER: 60/091633
65	PRIOR FILING DATE: 1998-07-02
66	PRIOR APPLICATION NUMBER: 60/091976
67	PRIOR FILING DATE: 1998-07-07
68	PRIOR APPLICATION NUMBER: 60/091982
69	PRIOR FILING DATE: 1998-07-07
70	PRIOR APPLICATION NUMBER: 60/092182
71	PRIOR FILING DATE: 1998-07-09

Query Match

7.78; Score 110.5; DB 9; Length 215;

Best Local Similarity 25.0%; Pred. No. 0.0047;
Matches 48; Conservative 29; Mismatches 78; Indels 37; Gaps 9;

```

QY 3 RLALVGAALVSSACGCVVDSE--TEAVYGMTEFKLICCKRSETNATETFTWTFR 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 8 RAVLLILGILQILALMPILAIVEITYSRVLEAVNGTDARLKTFFSFAVGDALIVT-MNFR 66
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 61 --QKGTSEFVKILRYENEVLQLEDEDFEGRVVWNGSRGTDLQDLSIFITNVTYNHSGD 118
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 67 PLDGGPEQV--FYHIDFQ--PMGGRFDRYSWDGN--PERYDASILLWKLQFDDNGT 120
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 119 YECHVYRLIFPENVEHNTSVVKIHIEVVDKGE-----SGACPFYV----- 161
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 121 YTCQV-----KNPPDVDDGIVGEIRLSVHTVRFSEIHFLALAISSACALMIIVIVVL 174
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 162 ---HRRARWRDR 170
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 175 FOHYRKGRWAER 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Search completed: January 29, 2003, 13:32:48
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:27:17 ; Search time 18 Seconds

(without alignments)
1431.335 Million cell updates/sec

Title: US-09-875-456a-14

Perfect score: 1444

Sequence: 1 MGRLLALVVGALVSSACGG.....QRRVIGLFGIIIRCVSRGVV 268

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	54.2	218	2 A55734	sodium channel, vo
2	751	52.0	218	2 A42737	sodium channel, bet
3	749	51.9	218	2 JC4788	sodium channel bet
4	110.5	7.7	246	1 A32999	myelin P0 protein
5	110.5	7.7	249	1 A61087	myelin P0 glycopro
6	107	7.4	369	2 JM0053	extracellular sign
7	100	6.9	248	1 MPRT0	myelin P0 protein
8	98.5	6.8	248	1 JH0252	myelin P0 protein
9	98.5	6.8	251	2 I38053	myelin protein zer
10	98	6.8	361	2 A36754	mitogen-activated
11	97.5	6.8	247	1 A54662	myelin P0 protein
12	94	6.5	358	2 S16444	mitogen-activated
13	94	6.5	358	2 A40033	protein kinase (EC
14	94	6.5	360	1 JQ1400	MAP kinase 1 (EC 2
15	94	6.5	360	2 S25011	protein kinase ERK
16	93	6.4	219	1 A29128	myelin P0 protein
17	92.5	6.4	1099	2 A59311	myosin VII, ZMM3
18	92	6.4	5175	2 T20892	hypothetical prote
19	92	6.4	5176	2 T43290	hemiscientific prote
20	91.5	6.3	4302	2 A38971	polycystic kidney
21	89.5	6.2	392	2 JM0052	extracellular sign
22	85.5	5.9	1337	2 T09402	immunoglobulin-lik
23	84	5.8	948	2 T03225	probable regulator
24	83.5	5.8	978	2 T16848	hypothetical prote
25	83	5.7	189	2 S49846	asparagine synthas
26	82	5.7	188	2 I59116	myc protein - huma
27	82	5.7	1120	2 T14275	myosin-like protei
28	81.5	5.6	376	2 A36978	MAP kinase mpk-1 (
29	81.5	5.6	444	2 A36977	MAP kinase sur-1 (

30	81.5	5.6	662	2 T16845	hypothetical prote
31	81	5.6	355	1 LKCH	proteoglycan link
32	81	5.6	670	1 A30882	arachidonate 5-lip
33	81	5.6	1088	1 PPRGTA	platelet-derived g
34	81	5.6	1155	2 G96539	hypothetical prote
35	79.5	5.5	482	2 T15333	hypothetical prote
36	79.5	5.5	822	2 B49151	fibroblast growth
37	79.5	5.5	1089	1 S33727	platelet-derived g
38	79.5	5.5	2135	2 T14602	variant-specific s
39	79	5.5	188	2 T19500	myc protein - huma
40	79	5.5	188	2 J00451	hypothetical 21k p
41	79	5.5	408	1 LKRT2	proteoglycan link
42	79	5.5	858	1 VCLJG2	env polypeptide pr
43	78.5	5.4	111	1 L6HULT	Ig lambda chain V-
44	78.5	5.4	300	2 T13535	N-acetylmuramoyl-L
45	78.5	5.4	352	2 S70580	activin beta C pre

ALIGNMENTS

RESULT 1

A55734

Sodium channel, voltage-gated, beta-1 chain precursor - human.

C/Species: Homo sapiens (man)

C/Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 08-Oct-1999

C/Accession: A55734; A53408; I54354

R/Makita, N.; Sloan-Brown, K.; Weghuis, D.O.; Ropers, H.H.; George Jr., A.L.

A/Title: Genomic organization and chromosomal assignment of the human voltage-gated Na(+)

A/Reference number: A55734; MUID:95154833; PMID:7851891

A/Accession: A55734

A/Molecule type: DNA

A/Residues: 1-218 <MAK1>

A/Cross-references: GB:U12189

R/Makita, N.; Bennett Jr., P.B.; George Jr., A.L.

J. Biol. Chem. 269, 7571-7578, 1994

A/Title: Voltage-gated Na(+) channel beta-1 subunit mRNA expressed in adult human skelet

A/Reference number: A53408; MUID:94171787; PMID:8125980

A/Accession: A53408

A/Molecule type: mRNA

A/Residues: 1-218 <MAK2>

A/Cross-references: GB:L16242; NID:9450602; PIDN:AAA61277.1; PID:9450603

R/McClatchey, A.I.; Cannon, S.C.; Slaugenhaupt, S.A.; Gusella, J.F.

Hum. Mol. Genet. 2, 745-749, 1993

A/Title: The cloning and expression of a sodium channel beta 1-subunit cDNA from human b

A/Reference number: I54354; MUID:93357746; PMID:8394762

A/Accession: I54354

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-218 <RES>

A/Cross-references: GB:L10338; NID:9307414; PIDN:AAA60391.1; PID:9307415

C/Genetics:

A/Gene: GDB:SCN1B

A/Cross-references: GDB:127281; OMIM:600235

A/Map position: 19q13.1-19q13.1

C/Keywords: glycoprotein; muscle; transmembrane protein

F.1-19/Domain: signal sequence #status predicted <SIG>

F.161-182/Domain: transmembrane #status predicted <TM>

F.193.110.114.135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 96.8%; Pred. No. 5.2e-63;

Matches 150; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MGRLLALVVGALVSSACGGCVCVDSSTETAYVGMFKILICISCKRRSTNAETFTWTFR 60
Db	1	MGRLLALVVGALVSSACGGCVCVDSSTETAYVGMFKILICISCKRRSTNAETFTWTFR 60
Qy	61	QKGTSEFVKILRYENRVLQLEDERFEGRVVWNGSRGTKDLDLISFTNTVYVNSGDYE 120
Db	61	QKGTSEFVKILRYENRVLQLEDERFEGRVVWNGSRGTKDLDLISFTNTVYVNSGDYE 120

QY 121 CHVYRLFFENYEHNTSVVKKIHLEVDKESGAA 155
 Db 121 CHVYRLFFENYEHNTSVVKKIHLEVDKANRDM 155

RESULT 2

A42737

sodium channel beta 1 subunit - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C/Accession: A42737

R/Isom: L.I.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa Science 256, 839-842, 1992

A/Title: Primary structure and functional expression of the beta 1 subunit of the rat br

A/Reference number: A42737; MUID:92271207; PMID:1375395

A/Accession: A42737

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid; protein

A/Residues: 1-218 <ISO>

A/Cross-references: GB:M91808; NID:g206864; PIDN:AAA8513.1; PID:g206865

A/Experimental source: Brain

A/Note: Sequence extracted from NCBI backbone (NCBIP:103298)

C/Keywords: transmembrane protein

Query Match 52.0%; Score 751; DB 2; Length 218;
 Best Local Similarity 92.9%; Pred. No. 4e-60;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 60
 Db 1 MGRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 60

QY 61 QKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVNHSGDYE 120
 Db 61 QKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVNHSGDYE 120

QY 121 CHVYRLFFENYEHNTSVVKKIHLEVDKESGAA 155
 Db 121 CHVYRLFFENYEHNTSVVKKIHLEVDKANRDM 155

QY 121 CHVYRLFFENYEHNTSVVKKIHLEVDKESGAA 155
 Db 121 CHVYRLFFENYEHNTSVVKKIHLEVDKANRDM 155

RESULT 3

JC4788

sodium channel protein beta 1 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C/Accession: JC4788

R/Belcher, S.M.; Howe, J.R. Gene 170, 285-286, 1996

A/Title: Cloning of the cDNA encoding the sodium channel beta 1 subunit from rabbit.

A/Reference number: JC4788; MUID:9625151; PMID:8666261

A/Accession: JC4788

A/Molecule type: mRNA

A/Residues: 1-218 <BEL>

A/Cross-references: GB:J35382; NID:g1016013; PIDN:AA81572.1; PID:g1016014

C/Comment: This protein is composed of a large alpha-chain and two small beta-chains and

duction.

C/Genetics:

A/Genes: Obeta1

C/Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

F:161-182/Domain: transmembrane #status predicted <TM>

F:99,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 749; DB 2; Length 218;
 Best Local Similarity 92.9%; Pred. No. 6e-60;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 60
 Db 1 MGRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 60

QY 61 QKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVNHSGDYE 120
 Db 61 QKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVNHSGDYE 120

Db 61 QKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVNHSGDYE 120
 QY 121 CHVYRLFFENYEHNTSVVKKIHLEVDKESGAA 155
 Db 121 CHVYRLFFENYEHNTSVVKKIHLEVDKANRDM 155

RESULT 4

A32999

myelin P0 protein precursor - horn shark

C/Species: Heterodontus francisci (horn shark)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C/Accession: A32999

R/Savedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, J. Mol. Evol. 29, 149-156, 1989

A/Title: The myelin proteins of the shark brain are similar to the myelin proteins of th

A/Reference number: A32999; MUID:90040744; PMID:2478717

A/Accession: A32999

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-246 <SNA>

A/Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:g4467434

A/Superfamily: myelin P0 protein; immunoglobulin homology

C/Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein

F:41-127/Domain: immunoglobulin homology <IM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021;
 Matches 30; Conservative 13; Mismatches 43; Indels 13; Gaps 3;

QY 53 TTEWTFQKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTVN 110
 Db 60 TLLSRFRPNDSPDRIISLFHNGVPIYIEKQGRGKVENWG-----DISKHDSIVIRN 114

QY 111 VTYNHSGDYECHYVRLFFENYEHNTSVVKKIHLEVDK 149
 Db 115 LDYIDNGTFTCDV-----KNPPDVGTSGSDVHLTVYDK 147

QY 111 VTYNHSGDYECHYVRLFFENYEHNTSVVKKIHLEVDK 149
 Db 115 LDYIDNGTFTCDV-----KNPPDVGTSGSDVHLTVYDK 147

RESULT 5

A61087

myelin P0 glycoprotein precursor - chicken

C/Species: Gallus gallus (chicken)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000

C/Accession: A61087

R/Bardu, M. J. Neurosci. Res. 25, 143-151, 1990

A/Title: Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for ean

A/Reference number: A61087; MUID:90204597; PMID:1690817

A/Accession: A61087

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-249 <BAR>

C/Comment: This protein is found only in peripheral nervous system Schwann cells.

C/Superfamily: myelin P0 protein; immunoglobulin homology

C/Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protei

F:1-28/Domain: signal sequence #status predicted <SIG>

F:30-249/Product: myelin P0 glycoprotein #status predicted <MAT>

F:130-153/Domain: extracellular #status predicted <EXT>

F:143-129/Domain: immunoglobulin homology <IM>

F:154-179/Domain: transmembrane #status predicted <TM>

F:180-249/Domain: intracellular #status predicted <INT>

F:112/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 7.7%; Score 110.5; DB 1; Length 249;
 Best Local Similarity 29.8%; Pred. No. 0.021;
 Matches 39; Conservative 23; Mismatches 50; Indels 19; Gaps 6;

QY 2 GRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 56
 Db 9 GRLLAVVGAALVSSACGCGVEVDSETEAVYGMFTKILICISCRRETAETFTETFR 61

QY 57 -----WTFQKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTV 112
 Db 57 -----WTFQKGTSEEVKILRYENEVLQLEDERFEGRVVWNGSGRTKLDLSIFITVTV 112

Db 62 ISYVWHFQAGSGRDSISIFHYGKGQPIDDVGSFKEMEVGNPRK---DGSIVIHNDL 118
 QY 113 YNHSGDYECV 123
 Db 119 YTDNGFTCDV 129

RESULT 6

JM0053
 extracellular signal-regulated kinase (BC 2.7.-.-) 2 - common carp

N/Alternate names: CERK2
 C/Species: Cyprinus carpio (common carp)

C/Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 02-Nov-2001

C/Accession: JM0053
 R/Hashimoto, H.; Yokoyama, Y.; Matsuo, Y.; Toyohara, H.; Kohno, M.; Sakaguchi, M.

J. Biochem. 123, 1031-1035, 1998
 A/Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.

A/Reference number: JM0052; PMID:98269030; PMID:9603989

A/Accession: JM0053

A/Molecule type: mRNA

C/Comment: This enzyme is the key enzyme in the intracellular signal transduction pathway
 C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: phosphotransferase
 F/32-322/Domain: protein kinase homology <KIN>

Query Match 7.4%; Score 107; DB 2; Length 369;

Best Local Similarity 19.1%; Pred. No. 0.068;
 Matches 61; Conservative 54; Mismatches 99; Indels 106; Gaps 16;

QY 9 VGALVSSAGCGCVSETEAVYGMFKI-----LCISCKRRSEPTNA 51
 Db 1 MATAAVAPRAGGCGNPGSGAEMVWGAFVDGPRRTNLSYIGBAGYCAVCAKRDKNRVY 60
 QY 52 -----EFFTEWTFPRQKTEEFVKILRYE-----NEVLQLEDEFEFEGRVNNGSRGK 99
 Db 61 AIKKISPEHQYQCRILREIKILRFKHNIIIGINDIITTTIDQMKDYVI-----VQ 114
 QY 100 DLDDLSFITNVTYNHSGDYECV-VYRLLPFENEHNTSVYKK-----IHIEV 146
 Db 115 DLNETDYLKILKTOHLSNDHICFELYILGLKTIHSANVLRDLKPSNILLMTTCDLKI 174
 QY 147 VDKGSGACPEFTVTRRARWRDQVADRTGMLCAMPAR---IQORAEGRSSPSCP 202
 Db 175 CDFGLAVADP---DH-----DHTGFLTEVAIRWRARHIMNSGYTSS-- 217
 QY 203 LQLM-----PLFLSPRRQSMVPHRRSGYFTOLCHLCMTSG-----RC 243
 Db 218 IDIWSVGCIIAEMLSNRPF-----FGKH-----YLDQNLHILGILSPSOEDLNC 263
 QY 244 LLSLSQR-VVLGPGILIRC 262
 Db 264 IINIKANVLLSLP---LRC 280

RESULT 7

MPRT0
 myelin P0 protein precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Feb-1995

C/Accession: J00622; A22822

R/Lemke, G.; Lamar, E.; Patterson, J.

A/Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.

A/Reference number: J00622; PMID:90166482; PMID:2483091

A/Accession: J00622

A/Molecule type: DNA

A/Residues: 1-248 <LEM>
 R/Lemke, G.; Axel, R.
 Cell 40, 501-508, 1985
 A/Title: Isolation and sequence of a cDNA encoding the major structural protein of periph
 A/Reference number: A22822; PMID:85124601; PMID:2578865

A/Accession: A22822
 A/Molecule type: mRNA
 A/Residues: 1-248 <LEM>
 C/Comment: This protein is found only in peripheral nervous system Schwann cells.

C/Genetics: 23/1; 78/3; 150/1; 195/2; 215/3

C/Superfamily: myelin P0 protein; immunoglobulin homology

C/Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protei

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-248/Product: myelin P0 protein #status predicted <MAT>

F/30-153/Domain: extracellular #status predicted <EXT>

F/154-179/Domain: immunoglobulin homology <IMM>

F/180-248/Domain: transmembrane #status predicted <TMD>

F/122/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.9%; Score 100; DB 1; Length 248;

Best Local Similarity 25.0%; Pred. No. 0.18;
 Matches 30; Conservative 21; Mismatches 65; Indels 4; Gaps 2;

QY 4 LIALVGAALVSSAGCGCVSETEAVYGMFKILCISCKRRSEPTNAETFEWTFRQK 63
 Db 14 LIALPSSLVLSPTLAIVYTDREYVAGVSGVTHCSFWSSEWSDISFT-WRYQSEG 72
 QY 64 TEEFVKILRYENEVLQLEDEFEFEGRVNNGSRGKTDLDLSIFITNVTYNHSGDYECV 123
 Db 73 GRDAISIFHYAGGOPYIDEVGVTFKRIQWGDPSMK---DGSIVIHNDYSDNGFTCDV 129

RESULT 8

JH0252
 myelin P0 protein precursor - human

N/Alternate names: myelin protein zero

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 06-Dec-1996 #text_change 16-Jun-2000

C/Accession: JH0252; JN0704; I39378; I58118

R/Hayasaka, K.; Nanao, K.; Tahara, M.; Saito, W.; Takada, G.; Miura, M.; Uyemura, K.

Biochem. Biophys. Res. Commun. 180, 515-518, 1991

A/Title: Isolation and sequence determination of cDNA encoding the major structural prot

A/Reference number: JH0252; PMID:92062068; PMID:1719967

A/Accession: JH0252

A/Molecule type: mRNA

A/Residues: 1-248 <HA2>

A/Cross-references: GB:D10537; GB:D90501; NID:g220073; PIDN:BAA01395.1; PID:g220074

A/Experimental source: fetus spinal cord

R/Hayasaka, K.; Ohishi, A.; Takada, G.; Fukushima, Y.; Murai, Y.

Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993

A/Title: Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy type 1.

A/Reference number: JN0704; PMID:9356807; PMID:7688964

A/Accession: JN0704

A/Molecule type: mRNA

A/Residues: 1-248 <HA2>

R/Pham-Dinh, D.; Fourbil, Y.; Bianquet, F.; Mattei, M.G.; Roeckel, N.; Latour, P.; Chaz

Hum. Mol. Genet. 2, 2051-2054, 1993

A/Title: The major peripheral myelin protein zero gene: structure and localization in ch

A/Reference number: J39378; PMID:94154677; PMID:7509228

A/Accession: J39378

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-248 <RES>

A/Cross-references: GB:L24893; NID:g454412; PIDN:AAA20656.1; PID:g529405

R/Kulkarni, T.; Bolhuis, P.A.; Wolterman, R.A.; Kemp, S.; de Nijenhuis, S.; Valentijn, L.

Nature Genet. 5, 35-39, 1993

A/Title: Deletion of the serine 34 codon from the major peripheral myelin protein P0 ge

A/Reference number: I58118; PMID:94035114; PMID:7693130

A/Accession: I58118

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-62, 64-115 <RE2>

A/Cross-references: GB:S66705; NID:g437048; PIDN:AAB28708.1; PID:g437049

A/Experimental source: disease-state mutant

C/Comment: This protein, a small integral membrane glycoprotein, is the most abundant pr

C/Comment: This protein plays essential roles in both the elaboration and the subsequent

C/Genetics:
 A:Gene: GDB:MP2; CMT1; CMT1B; HMSNB
 A:Cross-references: GDB:125266; OMIM:159440
 A:Map position: 1q22-1q23
 A:Introns: 23/1; 78/3; 150/1; 195/2; 215/3
 C:Superfamily: myelin P0 protein; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-248/Product: peripheral myelin #status predicted <PR>
 F:43-123/Domain: immunoglobulin homology <IMM>
 F:50-127/Dissulfide bonds: #status predicted
 F:122/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 98.5; DB 1; Length 248;
 Best Local Similarity 26.4%; Pred. No. 0.25; Indels 5; Gaps 3;
 Matches 32; Conservative 23; Mismatches 61; Indels 5; Gaps 3;

Qy 4 LLAIVGAAV-SSACGGCVDESETEAVYGMTFKILCISCKRSETNAETFTETPRK 62
 Db 13 ILAVLFSSVLPSPQAIVVYTDREHVGAVSRVTLHCSFMSSEWADDISFT-WRYQPE 71
 Qy 63 GTEEFVKLRLENVQLQEBDEPRGRVWNGSGRTKDLQDLSIFITNVYNNHSGDYEC 122
 Db 72 GGRDAISIFHYAKQOPYIDEVGTFRKRIQWVGDPWRK---DGSIVIHNDLSDNGFTPTCD 128

Qy 123 V 123
 Db 129 V 129

RESULT 9
 138053
 myelin protein zero - human
 C:Species: Homo sapiens (man)
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jan-2000
 C:Accession: 138053; A49643; S33191
 R:Rautenstrauss, B.; Nelis, E.; Grehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.
 Hum. Mol. Genet. 3, 1701-1702, 1994
 A:Title: Identification of a de novo insertional mutation in P0 in a patient with a Deje
 A:Reference number: 138053; MUID:55153453; PMID:7530550
 A:Accession: 138053
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-251 <RES>
 A:Cross-references: EMBL:Z31718; NID:9469516; PID:CA83513.1; PID:9469517
 R:Su, Y.; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993
 A:Title: Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients.
 A:Reference number: A49643; MUID:94068501; PMID:7504284
 A:Accession: A49643
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 50-105 <SU1>
 A:Experimental source: peripheral blood
 A:Note: sequence extracted from NCB1 backbone (NCB1P:139777)
 C/Genetics:
 A:Gene: GDB:MP2; CMT1B; CMT1
 A:Cross-references: GDB:125266; OMIM:159440
 A:Map position: 1q22-1q23
 C:Superfamily: myelin P0 protein; immunoglobulin homology
 F:43-123/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 98.5; DB 2; Length 251;
 Best Local Similarity 26.4%; Pred. No. 0.25; Indels 5; Gaps 3;
 Matches 32; Conservative 23; Mismatches 61; Indels 5; Gaps 3;

Qy 4 LLAIVGAAV-SSACGGCVDESETEAVYGMTFKILCISCKRSETNAETFTETPRK 62
 Db 13 ILAVLFSSVLPSPQAIVVYTDREHVGAVSRVTLHCSFMSSEWADDISFT-WRYQPE 71
 Qy 63 GTEEFVKLRLENVQLQEBDEPRGRVWNGSGRTKDLQDLSIFITNVYNNHSGDYEC 122
 Db 72 GGRDAISIFHYAKQOPYIDEVGTFRKRIQWVGDPWRK---DGSIVIHNDLSDNGFTPTCD 128

Qy 123 V 123
 Db 129 V 129

RESULT 10
 A39754
 mitogen-activated protein kinase (EC 2.7.1.1.-) - African clawed frog
 M:Alternate names: M phase MAP kinase
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 18-Jun-1999
 C:Accession: A39754; S16597
 R:Posada, J.; Sanphers, J.; Pelech, S.; Hebertsold, R.; Cooper, J.A.
 Mol. Cell. Biol. 11, 2517-2528, 1991
 A:Title: Tyrosine phosphorylation and activation of homologous protein kinases during o
 A:Reference number: A39754; MUID:91203872; PMID:1708093
 A:Accession: A39754
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-361 <POS>
 A:Cross-references: GB:M60977
 R:Gotch, Y.; Moriyama, K.; Matsuda, S.; Okumura, E.; Kishimoto, T.; Kawasaki, H.; Suzuki
 EMBO J. 10, 2661-2668, 1991
 A:Title: Xenopus M phase MAP kinase: isolation of its cDNA and activation by MPF.
 A:Reference number: S16597; MUID:91330892; PMID:174387
 A:Accession: S16597
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-4, 'G', 'A', '8-28', 'I', '30-31', 'A', '33-46', 'D', '48', 'V', '50-331', 'F', '333-361 <GOT>
 A:Cross-references: EMBL:X59813; NID:964893; PID:CA42482.1; PID:964894
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
 F:26-316/Domain: protein kinase homology <KIN>
 F:34-42/Region: protein kinase ATP-binding motif

Query Match 6.8%; Score 98; DB 2; Length 361;
 Best Local Similarity 20.1%; Pred. No. 0.43; Indels 94; Gaps 16;
 Matches 56; Conservative 49; Mismatches 80; Indels 94; Gaps 16;

Qy 29 EAVYGMTFKILC-----ISCKRSETNAETFTETPRKCTEEFVKIL---RYE----- 74
 Db 36 EGAYGVCSAHCNINKVVAIKISPFHQYQCTLR-----IKILRFKHNITGI 89
 Qy 75 NEVLQEBDEPRGRVWNGSGRTKDLQDLSIFITNVYNNHSGDYEC-VVRLFFENYE 133
 Db 90 NDIIRAPTEQMKDYI-----VQDLMETDYLKLTQHSNDHICFYLQILRGKLYT 143
 Qy 134 HNTSVVK-----IHIEVVDKGSAGACPFVTHRRARWRDRQAVDRGWL 181
 Db 144 HGANVLRHLRKLKSNLLMTTQDLKICDFGLARVADP---DH-----DHTGFLT 188
 Qy 182 AMPANR---PQRAEGSGSPSCPLQM-----PLFLSPRRGQSNPVPHR 224
 Db 189 EYVATRWYRAPRIMNSKGYTKS--IDIVSGCILAEMLSNRPIF-----PKR- 235
 Qy 225 RSGYRTOCHLCGCMTSG-----RCLLSLOR-VVLAGP 256
 Db 236 ---YLDQNLHILGIGSPSQEDLANCTINLKARNYLSLP 271

RESULT 11
 A54662
 myelin P0 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A54662
 R:Yon, K.H.; Hsieh, C.L.; Hayes, C.; Stahl, N.; Francke, U.; Popko, B.
 Genomics 9, 751-757, 1991
 A:Title: DNA sequence, genomic organization, and chromosomal localization of the mouse
 A:Reference number: A54662; MUID:91244320; PMID:1709914
 A:Accession: A54662
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-247 <YOU>
 A:Cross-references: GB:M62427
 C:Superfamily: myelin P0 protein; immunoglobulin homology
 F:43-128/Domain: immunoglobulin homology <IMM>

Query Match 6.5%; Score 97.5; DB 1; Length 247;
 Best Local Similarity 27.3%; Pred. No. 0.31;
 Matches 33; Conservative 20; Mismatches 61; Indels 7; Gaps 3;

QY 4 LIALVYGAALVSSACGGVEVDSETEAVYGMTPFKLICGRSEETAETFTETFR-OK 62
 DB 14 LIALFSSIVLSPALAIYVYTDRE---YGAAGSVTLHCFSSEWSDDISTFWYOE 70
 QY 63 GTEEVFKILRYENEVLQLEBDEFEGRVWNGSGRTKDLQDLISFITNVYNSGDYEC 122
 DB 71 GGRDAISIFHAKGOPYIDEVGAFFERIQWVGDPKWK---DGSIVINLDYSDNGTFTCD 127
 QY 123 V 123
 DB 128 V 128

RESULT 12

S16444
 Mitogen-activated protein kinase (EC 2.7.1.-) - mouse
 N:Alternate names: cell division cycle-2-related protein kinase ERK2
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
 C:Accession: S16444; S15015; P0480
 R:Her, J.H.; Wu, J.; Rall, T.B.; Stungill, T.W.; Weber, M.J.
 Nucleic Acids Res. 19, 3743, 1991
 A:Title: Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by tyrosine ph
 A:Reference number: S16444; MUID:91305126; PMID:1649458
 A:Accession: S16444

A:Molecule type: mRNA
 A:Residues: 1-358 <HER>
 A:Cross-references: EMBL:X58712; NID:G53001; PIDD:CA441548.1; PID:G53002
 A:Note: Part of this sequence was confirmed by protein sequencing
 R:Payne, D.M.; Rosomando, A.U.; Martino, P.; Erickson, A.K.; Her, J.H.; Shabanowitz, J.
 EMBO J. 10, 885-892, 1991
 A:Title: Identification of the regulatory phosphorylation sites in pp42/mitogen-activate
 A:Reference number: S15015; MUID:91184134; PMID:1849075
 A:Accession: S15015
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 171-181, 'X', 183-189 <PAY>
 R:Ernst, W.A.; Nagorskaya, T.V.; Vlasov, J.W.M.; Belyavsky, A.V.
 Gene 124, 305-306, 1993
 A:Title: Novel CDC2-related protein kinases produced in murine hematopoietic stem cells.
 A:Reference number: P0479; MUID:93185941; PMID:8444355
 A:Accession: P0480
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 145-195 <ERS>
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonin
 F:21-311/Domain: protein kinase homology <KIN>
 F:29-37/Region: protein kinase ATP-binding motif
 F:183/Binding site: phosphate (Thr) (covalent) #status experimental
 F:185/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 6.5%; Score 94; DB 2; Length 358;
 Best Local Similarity 20.1%; Pred. No. 0.98;
 Matches 57; Conservative 49; Mismatches 75; Indels 102; Gaps 17;

QY 29 EAVYGMTPFKLIC-----ISCKRSEETAETFTETFRQKGRSEVKIL---RYE- 74
 DB 31 EGAYGM-----VCSAYDNLKRVVAIKKISPFHQYTCQRTLE-----IKILNFRHEN 80
 QY 75 -----NEVLQLEBDEFEGRVWNGSGRTKDLQDLISFITNVYNSGDYEC-VRLLFF 129
 DB 81 IIGINDIIRAPTEIQMKDVI-----VDLMETDLYKLKTOHLSNDHICFVQIILRG 134

QY 130 ENYEHTSVYKK-----IHIEVDKGESSGAACPFTVTHRRARRDRNOAVDRT 177
 DB 135 LKTIHSANVLHRDLKPSNLLNTTCDLTCDFGLARVADP---DH-----DHT 179

QY 178 GWLCAMPANR-----POQRAEGSSPSCPLQLW-----PLFLSPRRGQSM 220
 DB 180 GLTEYVATFRWRAPEIMLNSKGYTKS--IDWSVGCILAEMLSNRPIF-----P 227

QY 221 VPHRSGYRTQCHLCMTSG-----RCLLSQR-VVLGLP 256
 DB 228 GKH-----YLDQLNHLIIGILGSPQEDLNCIINLKARNVLLSLP 266

RESULT 13

A40033
 Protein kinase (EC 2.7.1.37) ERK2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 18-Jun-1999
 C:Accession: A40033
 R:Boulton, T.G.; Nye, S.H.; Robbins, D.J.; Ip, N.Y.; Radziejewski, E.; Morgenbesser, S.D.
 Cell 65, 663-675, 1991
 A:Title: ERKs: a family of protein-serine/threonine kinases that are activated and tyros
 A:Reference number: A40033; MUID:91235302; PMID:2032290
 A:Accession: A40033
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <BOU>
 A:Cross-references: GB:M64300; NID:G204055; PIDD:AAA41124.1; PID:G204056
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
 F:21-311/Domain: protein kinase homology <KIN>
 F:29-37/Region: protein kinase ATP-binding motif

Query Match 6.5%; Score 94; DB 2; Length 358;
 Best Local Similarity 20.1%; Pred. No. 0.98;
 Matches 57; Conservative 49; Mismatches 75; Indels 102; Gaps 17;

QY 29 EAVYGMTPFKLIC-----ISCKRSEETAETFTETFRQKGRSEVKIL---RYE- 74
 DB 31 EGAYGM-----VCSAYDNLKRVVAIKKISPFHQYTCQRTLE-----IKILNFRHEN 80
 QY 75 -----NEVLQLEBDEFEGRVWNGSGRTKDLQDLISFITNVYNSGDYEC-VRLLFF 129
 DB 81 IIGINDIIRAPTEIQMKDVI-----VDLMETDLYKLKTOHLSNDHICFVQIILRG 134
 QY 130 ENYEHTSVYKK-----IHIEVDKGESSGAACPFTVTHRRARRDRNOAVDRT 177
 DB 135 LKTIHSANVLHRDLKPSNLLNTTCDLTCDFGLARVADP---DH-----DHT 179
 QY 178 GWLCAMPANR-----POQRAEGSSPSCPLQLW-----PLFLSPRRGQSM 220
 DB 180 GLTEYVATFRWRAPEIMLNSKGYTKS--IDWSVGCILAEMLSNRPIF-----P 227
 QY 221 VPHRSGYRTQCHLCMTSG-----RCLLSQR-VVLGLP 256
 DB 228 GKH-----YLDQLNHLIIGILGSPQEDLNCIINLKARNVLLSLP 266

RESULT 14

JQ1400
 MAP kinase 1 (EC 2.7.1.-) - human
 N:Alternate names: ERK; extracellular signal-regulated kinase 2 (ERK2); mitogen-activate
 N:Contains: protein kinase (EC 2.7.1.37)
 C:Species: Homo sapiens (man)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 11-Jun-1999
 C:Accession: JQ1400; S23426; S23427; S21577; S21578
 R:owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geyrhofer, T.D.
 Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992
 A:Title: Extracellular signal-regulated kinases in T cells: characterization of human ER
 A:Reference number: JQ1400; MUID:92171961; PMID:1540184
 A:Accession: JQ1400
 A:Molecule type: mRNA

A:Residues: 1-360 <GBA>
A:Cross-references: MB:04489; NID:G182190; PIDN:AAAS6459.1; PID:G182191
A:Experimental source: cell line Jurkat
F:Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
FEBS Lett. 304, 170-178, 1992
A:Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
A:Reference number: S23426; MUID:92316223; PMID:1339925
A:Accession: S23426
A:Molecule type: mRNA
A:Residues: 13-360 <GON1>
A:Cross-references: EMBL:Z11695; NID:G23878; PIDN:CAA77753.1; PID:G23878
A:Accession: S23427
A:Molecule type: mRNA
A:Residues: 1-30, 'Q', 92-360 <GON2>
A:Cross-references: EMBL:Z11694; NID:G23880; PIDN:CAA77752.1; PID:G23881
C:Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).
C:Genetics:
A:Gene: GDB:PRKML; ERK; MAPK1; ERK2
A:Cross-references: GDB:135677; OMTM:176948
A:Map position: 22q11.2-22q11.2
C:Complex: monomer
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: MAP kinase cascade
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:23-313/Domain: protein kinase homology <KIN>
F:13-39/Region: protein kinase ATP-binding motif
F:185/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted
F:187/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

Query Match	6.5%	Score 94;	DB 1;	Length 360;
Best Local Similarity	20.1%;	Pred. No. 0.98;		
Matches	57;	Conservative	49;	Mismatches 75;
				Indels 102;
				Gaps 17;

```

Qy 29 EAVNGMFKILC-----ISKRSSEMTAFEMTFROKGTBEFKIL--RYE- 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 EGAYGM---VCSAYDVNKKRAVAKIKSPIENHTYOCRLRE-----IKILRRPHEN 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 75 ---NEVLQLEDERFEGRVVWNGSRGTDLODISITITVNTYHSGDYCH--VYRLLF 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 IIGINDIRAPETIQMKDVIY-----VODLMEIDLKILKTOHLSNDHCYFYOLRG 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 130 ENYEHTNSVYVK-----IHIEVVDKGESGACPEVTYHRBARDRMQAVDRT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 LKTYHSANVLRDLKPSULLNTTCIDKICPGLARVADP---DH-----DHT 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 178 GMLCAMPANR-----POQRAEGSGSPSCPIOLW-----PLFUSPRGSGMP 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GFLTEYVATRWYRAPEIMNSKGTYKS--IDIWSGCILAEMLSNRPIF-----P 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 VPHRSGRYQIUCHLCMTSG-----RCILSLSOR--VVLGLP 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 GRH---YVDQNLNHLGLIGLSBQDCELDCLNLRKRNLYSLP 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 15
S25011
protein kinase ERK2 (RC 2.7.1.-) - bovine
N|Alternate names: extracellular signal-regulated kinase
C|Species: Bos primigenius taurus (cattle)
C|Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
C|Accession: S25011
R|Ely, C.M.; Cox, M.E.; Her, J.; Parsons, S.U.
Submitted to the EMBL Data Library, July 1992
A|Description: Cloning and sequencing of ERK2 from a bovine adrenal medulla cDNA library
A|Reference number: S25011
A|Accession: S25011
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-360 <Ely>
A|Cross-references: EMBL:Z14089; NID:g336; PIDD:CAA78467.1; PID:g337
C|Superfamily: Kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase F; 23-313/Domain: protein kinase homology <KIN> F; 31-39/Region: protein kinase ATP-binding motif

Query Match	6.54	Score 94	DB 2	Length 360
Best Local Similarity	20.1%	Pred. No. 0.98		
Matches 57; Conservative	49	Mismatches 75	Indels 102	Gaps 17

```

QY 29 EAVGMFKILC-----ISCKRSTNMTETEMFRQKTEFEVKIL--RYE- 74
      |||||
Db 33 EGAIGM---VCSAYDVNKKYRAVAKIKISPFHQYCOQRTLR-----IKILLRPFHEN 82
      |||||
QY 75 ----NEVLQLEDERFEFGVWVNGSRETQLODLSTFTVTVNHSQDECH-VYRLTF 129
      |||||
Db 83 IIGINDIRFPIETQMDDVI-----VDIMETIDYKLLKTLQHLSDNDHCYFLYDLNG 136
      |||||
QY 130 ENYEINTNSVVK-----IHLEVDKESGACPFVTHSRARWRDWCADVRT 177
      |||||
Db 137 LKTHISANVLRDLKPSNLNLNTTCDLTKIDPGLARVADP---DH-----DHT 181
      |||||
QY 178 GMLCAMPANR---POORABEGSGSPSCPIQLW-----PLFISSPRGOSMP 220
      |||||
Db 182 GFLTEYVATRWYRAPBEIMNSKGYTKS--IDIVSVCILAEMLSNREIF-----P 229
      |||||
QY 221 VPHRRSGYRTOQLCHCMTSG-----RCLISLQR--VVLGLP 256
      |||||
Db 230 GGN---YLDQNLHLGLGSSPSEDNLNCIINLKARUYLLSLP 268
      |||||

```

Search completed: January 29, 2003, 13:29:38
Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 13:24:27 ; Search time 11 Seconds

(without alignments)
1010.514 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444
Sequence: 1 MGRLLALVGAALVSSACGG.....QRYVLGPIIIRCVSRGVV 268

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	54.2	218	1 CIB1_HUMAN	O07699 homo sapien
2	752	52.1	218	1 CIB1_MOUSE	P97952 mus musculus
3	751	52.0	218	1 CIB1_RAT	Q00954 rattus norv
4	749	51.9	218	1 CIB1_RABIT	P53788 oryctolagus
5	258.5	17.9	215	1 CIB3_HUMAN	Q9ny72 homo sapien
6	114.5	7.9	215	1 EVAL_MOUSE	O70255 mus musculus
7	110.5	7.7	215	1 EVAL_HUMAN	O60487 homo sapien
8	110.5	7.7	246	1 MYPO_HERFR	P20938 heterodonta
9	110.5	7.7	249	1 MYPO_CHICK	P37301 gallus gall
10	101	7.0	248	1 MYPO_MOUSE	P27573 mus musculus
11	100	6.9	248	1 MYPO_RAT	P06907 rattus norv
12	98.5	6.8	248	1 MYPO_HUMAN	P26696 xenopus lae
13	98	6.8	361	1 MK01_XENTIA	P25189 homo sapien
14	94	6.5	181	1 BY55_HUMAN	P27703 homo sapien
15	94	6.5	358	1 MK01_MOUSE	P46156 bos taurus
16	94	6.5	360	1 MK01_BOVIN	P28482 homo sapien
17	94	6.5	360	1 MK01_BOVIN	P28482 homo sapien
18	93	6.4	219	1 MYPO_BOVIN	P10522 bos taurus
19	91	6.3	501	1 Z325_HUMAN	O9u166 homo sapien
20	90.5	6.3	4303	1 PKD1_HUMAN	P98161 homo sapien
21	81.5	5.6	444	1 SUR1_HUMAN	P39745 caenorhabdi
22	81.5	5.6	659	1 YRM3_CAEEL	O09353 caenorhabdi
23	81	5.6	355	1 PLK_CHICK	P07354 gallus gall
24	81	5.6	672	1 LOXS_RAT	P12527 rattus norv
25	81	5.6	1088	1 PGDS_RAT	P20786 rattus norv
26	80	5.5	664	1 PD13_SHEEP	O02849 ovis aries
27	79.5	5.5	215	1 CIB2_HUMAN	O60939 homo sapien
28	79	5.5	354	1 PLK_RAT	P03994 rattus norv
29	78.5	5.4	111	1 LV6D_HUMAN	P06510 homo sapien
30	78.5	5.4	352	1 THCB_MOUSE	P55104 mus musculus
31	78	5.4	356	1 PLK_MOUSE	O9qnp5 mus musculus
32	78	5.4	757	1 RRP1_TALE2	P26120 influenza a
33	78	5.4	757	1 RRP1_TALE3	P26121 influenza a

34	77.5	5.4	887	1 ORP3_HUMAN	Q9h415 homo sapien
35	77	5.3	382	1 GSP1_PSEAR	P25060 pseudomonas
36	77	5.3	457	1 CD4_RAT	P05540 rattus norv
37	77	5.3	757	1 RRP1_TALE1	P26119 influenza a
38	76.5	5.3	460	1 HEMO_MOUSE	O91x72 mus musculus
39	76	5.3	215	1 CIB2_RAT	P54900 rattus norv
40	76	5.3	365	1 CXAR_HUMAN	P78310 homo sapien
41	76	5.3	650	1 M110_CAEEL	P34400 caenorhabdi
42	76	5.3	672	1 LOXS_MESAU	P51399 mesocricetu
43	76	5.3	673	1 LOXS_MOUSE	P48999 mus musculus
44	76	5.3	858	1 ENV_HVZRO	P04577 human immun
45	75.5	5.2	417	1 PGCB_FELCA	P41725 felis silve

ALIGNMENTS

RESULT 1
CIB1_HUMAN STANDARD; PRT; 218 AA.
AC O07699;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN SCN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93357746; PubMed=8394762;
RA McClatchey A.I., Cannon S.C., Slangenbaup S.A., Gusejla J.F.;
RT "The cloning and expression of a sodium channel beta 1-subunit cDNA
from human brain.";
RL Hum. Mol. Genet. 2:745-749 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Heart;
RX MEDLINE=9417187; PubMed=8125980;
RA Makita N., Bennett P.B. Jr., George A.L. Jr.;
RT "Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult
human skeletal muscle, heart, and brain is encoded by a single
gene.";
RL J. Biol. Chem. 269:7571-7578 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95154833; PubMed=7851891;
RA Makita N., Sloan-Brown K., Weghuis D.O., Rogers H.H.,
RT George A.L. Jr.;
RT "Genomic organization and chromosomal assignment of the human
voltage-gated Na+ channel beta 1 subunit gene (SCN1B).";
RL Genomics 23:628-634 (1994).
RN [4]
RP VARIANT GEPS+ TRP-121.
RX MEDLINE=98361163; PubMed=9697698;
RA Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr.,
RA Phillips H.A., Saar K., Reis A., Johnson E.W., Sutherland G.R.,
RA Berkovic S.F., Mulley J.C.;
RT "Febrile seizures and generalized epilepsy associated with a mutation
in the Na(+)-channel beta-1 subunit gene SCN1B.";
RL Nat. Genet. 19:366-370 (1998).
-1- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL
MODULATION OF THE HETEROMERIC COMPLEX OF THE SODIUM CHANNEL.
THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT
ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART.
-1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA
SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY
ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
DISULFIDE BONDS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN SKELETAL MUSCLE, HEART
 CC AND BRAIN.
 CC -1- DISEASE: DEFECTS IN SCN1B ARE A CAUSE OF GENERALIZED EPILEPSY WITH
 CC FEBRILE SEIZURES PLUS (GEFS+), A DISEASE CHARACTERIZED BY A
 CC HIGHLY VARIABLE PHENOTYPE COMBINING FEBRILE SEIZURES, GENERALIZED
 CC SEIZURES OFTEN PRECIPITATED BY FEVER AT AGE 6 YEARS OR MORE, AND
 CC PARTIAL SEIZURES, WITH A VARIABLE DEGREE OF SEVERITY.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC
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 CC
 CC EMBL: L10338; AAC60391.1; -;
 CC EMBL: L16242; AAC61277.1; -;
 CC EMBL: U12193; AAB97608.1; -;
 CC EMBL: U12189; AAB97608.1; JOINED.
 CC EMBL: U12190; AAB97608.1; JOINED.
 CC EMBL: U12191; AAB97608.1; JOINED.
 CC EMBL: U12192; AAB97608.1; JOINED.
 CC EMBL: U12193; AAB97608.1; JOINED.
 CC GeneW: HGNC:10586; SCN1B.
 CC MIM: 600235; -;
 CC MIM: 604233; -;
 CC InterPro: IPR003006; IG_MHC.
 CC InterPro: IPR003600; IG_Like.
 CC Pfam: PF00047; Ig_1.
 CC SMART: SM00410; Ig_Like; 1.
 CC DR
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Signal; Immunoglobulin domain; Disease mutation.
 CC FT SIGNAL 1 18
 CC FT CHAIN 1 218
 CC FT DOMAIN 19 160
 CC FT TRANSMEM 161 182
 CC FT DOMAIN 183 218
 CC FT DISULFID 40 121
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 110 110
 CC FT CARBOHYD 114 114
 CC FT CARBOHYD 135 135
 CC FT VARIANT 121 121
 CC FT
 CC SQ SEQUENCE 218 AA; 24707 MW; 09B812F3F9E9018 CRC64;
 CC
 CC Query Match 54.2%; Score 783; DB 1; Length 218;
 CC Best Local Similarity 96.8%; Pred. No. 1,1e-65;
 CC Matches 150; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 CC
 CC QY 1 MGRLLAVGALVSSAGCGVEVDSETEAVYGMTPFKILICISCKRRSETNAETFTETWTFR 60
 CC DB 1 MGRLLAVGALVSSAGCGVEVDSETEAVYGMTPFKILICISCKRRSETNAETFTETWTFR 60
 CC QY 61 QKGTSEFVKILRYENEVLQLEDERFEGRRVWNGSGRTKLDLISFITVTVNHSGDYE 120
 CC DB 61 QKGTSEFVKILRYENEVLQLEDERFEGRRVWNGSGRTKLDLISFITVTVNHSGDYE 120
 CC QY 121 CHVRLLEFFENYENTSVVKKIHLEVDKESGAA 155
 CC DB 121 CHVRLLEFFENYENTSVVKKIHLEVDKESGAA 155
 CC DB 121 CHVRLLEFFENYENTSVVKKIHLEVDKESGAA 155
 CC
 CC RESULT 2
 CC CIBL_MOUSE STANDARD; PRT; 218 AA.
 CC AC P97952;
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium channel beta-1 subunit precursor.
 CN SCN1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=97165884; PubMed=9013777;
 RA Grosson C.L.S., Cannon S.C., Corey D.P., Gussella J.F.;
 RT "Sequence of the voltage-gated sodium channel beta1-subunit in
 RT wild-type and in quivering mice."
 RL Brain Res. Mol. Brain Res. 42:222-226(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98387156; PubMed=9721701;
 RA Kuperahmidt S., Yang T., Roden D.M.;
 RT "Modulation of cardiac Na+ current phenotype by beta1-subunit
 RT expression."
 RL Circ. Res. 83:441-447(1998).
 CC -1- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL
 CC MODULATION OF THE HETEROTRIMERIC COMPLEX OF THE SODIUM CHANNEL.
 CC THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT
 CC ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART (BY SIMILARITY).
 CC -1- SUBUNIT: THE SODIUM CHANNEL, CONSISTS OF A PORE-FORMING ALPHA
 CC SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY
 CC ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
 CC DISULFIDE BONDS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC
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 CC
 CC EMBL: U46681; AAC53006.1; -;
 CC EMBL: U85786; AAB49368.1; -;
 CC MGD: MGI:98247; Scn1b.
 CC InterPro: IPR003006; IG_MHC.
 CC InterPro: IPR003600; IG_Like.
 CC Pfam: PF00047; Ig_1.
 CC SMART: SM00410; Ig_Like; 1.
 CC DR
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Signal; Immunoglobulin domain.
 CC FT SIGNAL 1 18
 CC FT CHAIN 1 218
 CC FT DOMAIN 19 160
 CC FT TRANSMEM 161 182
 CC FT DOMAIN 183 218
 CC FT DISULFID 40 121
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 110 110
 CC FT CARBOHYD 114 114
 CC FT CARBOHYD 135 135
 CC FT
 CC SQ SEQUENCE 218 AA; 24650 MW; 5198F383B0A8C45 CRC64;
 CC
 CC Query Match 52.1%; Score 752; DB 1; Length 218;
 CC Best Local Similarity 92.9%; Pred. No. 8,7e-63;
 CC Matches 144; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 CC
 CC QY 1 MGRLLAVGALVSSAGCGVEVDSETEAVYGMTPFKILICISCKRRSETNAETFTETWTFR 60
 CC DB 1 MGRLLAVGALVSSAGCGVEVDSETEAVYGMTPFKILICISCKRRSETNAETFTETWTFR 60
 CC QY 61 QKGTSEFVKILRYENEVLQLEDERFEGRRVWNGSGRTKLDLISFITVTVNHSGDYE 120
 CC DB 61 QKGTSEFVKILRYENEVLQLEDERFEGRRVWNGSGRTKLDLISFITVTVNHSGDYE 120

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|||||
Db 61 OKGTEEFVKILRYENEVLQLEEDERFEGRVWNGSRGTDLQDLSIFITNVTYNSGDYE 120
Qy 121 CHVYRLFFENYEHTSVVKKIHIEVDKESGAA 155
Db 121 CHVYRLFFENYEHTSVVKKIHIEVDKESGAA 155

RESULT 3
CIB1_RABIT STANDARD; PRT; 218 AA.
AC 000954:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN SCN1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX MEDLINE=92271207; PubMed=1375395;
RA Iacon L.L., De Jongh K.S., Patton D.E., Reber B.F.X., Offord J.,
RA Chabouneau H., Walsh K., Goldin A.L., Caterall W.A.;
RT "Primary structure and functional expression of the beta 1 subunit of
RT the rat brain sodium channel.";
RL Science 256:839-842(1992)

-1- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL
MODULATION OF THE HETEROTRIMERIC COMPLEX OF THE SODIUM CHANNEL.
CC THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT
CC ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART.
CC -1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA
CC SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY
CC ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, SKELETAL MUSCLE,
CC AND SPINAL CORD.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC -----
DR EMBL; M91808; AAA88513.1; -
DR PIR; A42737; A42737.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003600; IG_1like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00410; IG_1like; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Signal; Immunoglobulin domain.
FT SIGNAL 1 18
FT CHAIN 1 18
FT DOMAIN 19 218 SODIUM CHANNEL BETA-1 SUBUNIT.
FT TRANSSEM 161 182 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 161 182 POTENTIAL.
FT DOMAIN 183 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 150 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 121 POTENTIAL.
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 218 AA; 24692 MW; 0BA84FC44FF2306B CRC64;

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Query Match 52.0%; Score 751; DB 1; Length 218;
Best Local Similarity 92.9%; Pred. No. 1,1e-62;
Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRLLALVGAALVSSACGGCVVDSETEAVYGMTKILICISKRKRSSTNAETFTWTFR 60
Db 1 MGTLLALVGAALVSSACGGCVVDSETEAVYGMTKILICISKRKRSSTNAETFTWTFR 60

Qy 61 OKGTEEFVKILRYENEVLQLEEDERFEGRVWNGSRGTDLQDLSIFITNVTYNSGDYE 120
Db 61 OKGTEEFVKILRYENEVLQLEEDERFEGRVWNGSRGTDLQDLSIFITNVTYNSGDYE 120

Qy 121 CHVYRLFFENYEHTSVVKKIHIEVDKESGAA 155
Db 121 CHVYRLFFENYEHTSVVKKIHIEVDKESGAA 155

RESULT 4
CIB1_RABIT STANDARD; PRT; 218 AA.
AC P53788;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium channel beta-1 subunit precursor.
GN SCN1B.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX MEDLINE=96235151; PubMed=8666261;
RA Belcher S.M., Howe J.R.;
RT "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
RT rabbit.";
RL Gene 170:285-286(1996).
CC -1- FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL
MODULATION OF THE HETEROTRIMERIC COMPLEX OF THE SODIUM CHANNEL.
CC THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT
CC ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART.
CC -1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA
CC SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY
CC ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC -----
DR EMBL; U35382; AAB17572.1; -
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003600; IG_1like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00410; IG_1like; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Signal; Immunoglobulin domain.
FT SIGNAL 1 18
FT CHAIN 1 18
FT DOMAIN 19 218 SODIUM CHANNEL BETA-1 SUBUNIT.
FT TRANSSEM 161 182 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 161 182 POTENTIAL.
FT DOMAIN 183 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 150 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 121 POTENTIAL.
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 218 AA; 24706 MW; 39BD17A1FAEF7D2 CRC64;

Query Match 51.9%; Score 749; DB 1; Length 218;
 Best Local Similarity 92.9%; Pred. No. 1.7e-62;
 Matches 144; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGILLALVGAALVSSACGCGVDSSTEVYGMTEFKLICISKRSENAETFTWTR 60
 DB 1 MGILLAFVGAALVSSACGCGVDSSTEVYGMTEFKLICISKRSENAETFTWTR 60
 QY 61 QKGTSEPVKILRYENEVLQLEEDERFEGRVVNGSRGTQDLSIFITVYVHSGDYE 120
 DB 61 QKGTSEPVKILRYENEVLQLEEDERFEGRVVNGSRGTQDLSIFITVYVHSGDYQ 120
 QY 121 CHVYRLFPENYEHTSVVKKIHIEVVDKESGAA 155
 DB 121 CHVYRLFPENYEHTSVVKKIHIEVVDKESGAA 155

RESULT 5
 CIB3 HUMAN STANDARD; PRT; 215 AA.

AC 09NY72;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium channel beta-3 subunit precursor.
 GN SCN3B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=20160948; PubMed=1068874;
 RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
 RA Pincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;
 RT "Beta3: an additional auxiliary subunit of the voltage-sensitive
 sodium channel that modulates channel gating with distinct kinetics.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).

RN SEQUENCE FROM N.A.
 RP TISSUE=Amalgam;
 RC MEDLINE=21154917; PubMed=11230166;
 RA Wleemann S., Weil B., Wellenreuther R., Gaassenhuber J., Glassl S.,
 RA Ansoer W., Boescher M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Mewes H.-W., Oltmanns B., Obermaier B., Tampe J., Heubner D.,
 RA Wambolt R., Korn B., Klein M., Pouset A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).

CC -1- FUNCTION: MODULATES CHANNEL GATING KINETICS.
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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DR EMBL; AJ243396; CAB76825.1; -
 DR EMBL; AL136589; CAB6524.1; -
 DR HSSP; P06907; INEU.
 DR InterPro; IPR003599; IG.

DR InterPro; IPR003066; IG_MHC.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Signal; Immunoglobulin domain.
 FT SIGNAL 1 22
 FT CHAIN 23 215
 FT DOMAIN 23 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 215
 FT DOMAIN 32 154
 FT DISULFID 45 120
 FT CARBOHYD 95 95
 FT CARBOHYD 109 109
 FT CARBOHYD 113 113
 FT CARBOHYD 121 121

SQ SEQUENCE 215 AA; 24702 MW; 70FC604B9E26662 CRC64;
 Query Match 17.9%; Score 258.5; DB 1; Length 215;
 Best Local Similarity 43.2%; Pred. No. 6.7e-17;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 5 LALVGAALVSSACGCGVDSSTEVYGMTEFKLICISKRSENAETFTWTRQKGT 64
 DB 10 LALVLIYVSVCPVCEVPSSTEVYGMTEFKLICISKRSENAETFTWTRVPEEGV 69

QY 65 EEFVKILRYENEVLQLEEDERFEGRVVNGSRGTQDLSIFITVYVHSGDYECHV 124
 DB 70 KDFLITYRNGHGVESPP--FQGRLOMGS--KDIDVSIYLVNTLNDSDGYITNVS 123
 QY 125 RLFPENYEHTSVVKKIHIEVVDK-GE 151
 DB 124 REFPEARHPVKTTRRLPLRTEAGE 151

RESULT 6
 EVAL MOUSE STANDARD; PRT; 215 AA.

AC 070255;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial V-like antigen 1 precursor.
 GN EVAL OR EVA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.
 RP STRAIN=RAG-2; TISSUE=Thymus;
 RC MEDLINE=98252857; PubMed=9585423;
 RA Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
 RA Martiani M., Teesalu T., Conauez G.G., Grassi F.,
 RT "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin
 RT superfamily, expressed in embryonic epithelia with a potential role as
 RT homeotypic adhesion molecule in thymus histogenesis.";
 RL J. Cell Biol. 141:1061-1071(1998).

CC -1- FUNCTION: Mediates homophilic cell-cell adhesion.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (probable).
 CC -1- TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis
 CC but not in thymocytes, lymphocytes, macrophage or dendritic cells
 CC or cell lines.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

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Fri Jan 31 07:51:23 2003

DR EMBL: AF030454; AAC40128.1; --
 DR HSSP: P06907; INED.
 DR MGD; MG1:1289160; EVA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
 KW Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 215
 FT DOMAIN 27 215
 FT TRANSMEM 155 175
 FT DOMAIN 176 215
 FT DOMAIN 40 130
 FT DISULFID 47 123
 FT CARBOHYD 39 123
 FT CARBOHYD 118 118
 SQ SEQUENCE 215 AA; 24162 MW; P685B36787CE69D5 CRC34;
 Query Match
 Best Local Similarity 7.9%; Score 114.5; DB 1; Length 215;
 Matches 49; Conservative 29; Mismatches 83; Indels 37; Gaps 9;

QY 4 LIALVVGALVSSAGGCVSE--DSEAVYGMFTKILICICKRRSETNAETFTWTRQ 61
 DB 9 VLPPLISQLTALCTPEAVEIYTSGLAVALVGTDLRLCTPSSPAVGDALTV--NNFRP 67
 QY 62 K--GTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTLODLSFITNVTYNNHSGDY 119
 DB 68 RDGGEGQFV--FYVHMDFR--PMSGRFKDRVSWDN--PERYVVS--LWKMLQDPDDNGTY 121
 QY 120 ECHVYRLFFENYEHNSTVKKIHIEVD-----KESGACPFVT----- 161
 DB 122 TCQV-----KNPDPVDGLVGTIRLSVHTVRFSEIYFLAVALSACALMIIVIVVL 175
 QY 162 --HRRARWRDRQAVDR 177
 DB 176 QHFRKKWADRADKAEGR 193

RESULT 7
 EVAL HUMAN STANDARD; PRT; 215 AA.
 AC 060487;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial V-like antigen 1 precursor.
 GN EVAL OR EVA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Spleen;
 RX MEDLINE=98252857; PubMed=9585423;
 RA Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
 RA Mariani M., Tessa T., Conale G.G., Grassi F.,
 RA Epithelial V-like antigen (EVA), a novel member of the immunoglobulin
 RT superfamily, expressed in embryonic epithelia with a potential role as
 RT homocytic adhesion molecule in thymus histogenesis.";
 RT J. Cell Biol. 141:1061-1071(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrial tumor;
 RA Davenport U.W., Neale G.A.M., Gootra R.M.;
 RT Identification of putative target genes involved in LMO2-induced
 RT leukemogenesis.";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=squamous cell carcinoma;
 RA Picetas A., Petersen I., Schlens K., Petersen S.;
 RT "Human EVA gene which is downregulated in lung carcinoma cells";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 CC - FUNCTION: Mediates homophilic cell-cell adhesion.
 CC - SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC - TISSUE SPECIFICITY: Expressed in thymocytes and thymic stromal
 CC cells; expression elevated in some T cell leukemias.
 CC - SIMILARITY: CONAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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DR EMBL: AF030455; AAC39762.1; --
 DR EMBL: AF275945; AAF87240.1; --
 DR EMBL: AF304447; AAF87240.1; --
 DR EMBL: BC017774; AAH17774.1; --
 DR HSSP: P06907; INED.
 DR Gene; HGNC:3496; EVA1.
 DR MIM; 604873; --
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
 KW Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 215
 FT DOMAIN 27 215
 FT TRANSMEM 155 175
 FT DOMAIN 176 215
 FT DOMAIN 40 130
 FT DISULFID 47 123
 FT CARBOHYD 39 123
 FT CARBOHYD 118 118
 SQ SEQUENCE 215 AA; 24484 MW; 9D19EBA798B5815A CRC64;

Query Match
 Best Local Similarity 7.7%; Score 110.5; DB 1; Length 215;
 Matches 48; Conservative 29; Mismatches 78; Indels 37; Gaps 9;

QY 3 RLIALVVGALVSSAGGCVSE--TEAVYGMFTKILICICKRRSETNAETFTWTR 60
 DB 8 RAVLLISQLTALCTPEAVEIYTSGLAVALVGTDLRLCTPSSPAVGDALTV--NNFR 66
 QY 61 --QKTEEFVKILRYENEVLQLEDERFEGRVVWNGSRGTLODLSFITNVTYNNHSGD 118
 DB 67 PLGGEGQFV--FYVHMDFR--PMSGRFKDRVSWDN--PERYVVS--LWKMLQDPDDNGT 120
 QY 119 ECHVYRLFFENYEHNSTVKKIHIEVDKGE-----SGACPFVT----- 161
 DB 121 YTCQV-----KNPDPVDGLVGTIRLSVHTVRFSEIYFLAVALSACALMIIVIVVL 174
 QY 162 --HRRARWRDR 170
 DB 175 FQHYKKRWAE 186

RESULT 8
 MYPO HETFR STANDARD; PRT; 246 AA.
 ID MYPO HETFR
 AC P20938;
 DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
 protein) (MPP)
 OS Heterodontus francisci (Horn shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Heterodontidae; Heterodontiformes;
 OC Heterodontidae; Heterodontus.
 NC NCB1_TaxID=7792;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90040744; PubMed=2478717;
 RA Saavedra R.A., Fors L., Abersold R.H., Arden B., Horvath S.,
 RA Sanders J., Hood L.;
 RT "The myelin proteins of the shark brain are similar to the myelin
 proteins of the mammalian peripheral nervous system.";
 RL J. Mol. Evol. 29:149-156(1989).
 CC -1- FUNCTION: CREATION OF AN EXTRACELLULAR MEMBRANE FACE WHICH GUIDES
 CC THE WRAPPING PROCESS AND ULTIMATELY COMPACTS ADJACENT LAMELLAE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND ONLY IN PERIPHERAL NERVOUS SYSTEM
 CC SCHWANN CELLS.
 CC -1- PFM: N-GLYCAN IS SULFATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN P0 PROTEIN FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X16714; CAB37865.1; -
 DR PIR: A32999; A32999.
 DR HSSP: P06907; INEU.
 DR InterPro: IPR003596; Ig_V.
 DR InterPro: IPR000920; Myelin_P0.
 DR PRINTS: PR00213; MYELINP0.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00568; MYELIN_P0; 1.
 DR Myelin; Structural protein; Transmembrane;
 KW Phosphorylation; Immunoglobulin domain; Signal.
 KM SIGNAL 1 27
 FT CHAIN 28 246 MYELIN P0 PROTEIN.
 FT DOMAIN 28 150 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 151 178 POTENTIAL.
 FT DOMAIN 179 246 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 48 125 POTENTIAL.
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (COMPLEX) (BY
 FT SIMILARITY).
 SQ SEQUENCE 246 AA; 27335 MW; A776A9ED9D430FA0 CRC64;
 Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.0045; Indels 13; Gaps 3;
 Matches 30; Conservative 13; Mismatches 43;
 QY 53 TTFETPRQKTEEFVKILRYENEVLQLEDEFEGRVWNGSRGTDL--ODLSIFITN 110
 DB 60 TTLSMRPRPNDSRDIIISIFHYGNGVPIEKQGFGRGVEVVG-----DISKIDGSLIVNN 114
 QY 111 VTYNHSGDYECVYRLIFENYEHTNSVVKIHIIEVVDK 149
 DB 115 LDYIDNGTFTCDV-----KNPPDVGTSSDVHLTVYDK 147
 RESULT 9
 MYPO_CHICK STANDARD; PRT; 249 AA.
 AC P37301;
 DE 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
 protein) (MPP).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90204597; PubMed=1690817;
 RA Barbu M.;
 RT "Molecular cloning of cDNAs that encode the chicken P0 protein:
 RT evidence for early expression in avians.";
 RL J. Neurosci. Res. 25:143-151(1990).
 CC -1- FUNCTION: CREATION OF AN EXTRACELLULAR MEMBRANE FACE WHICH GUIDES
 CC THE WRAPPING PROCESS AND ULTIMATELY COMPACTS ADJACENT LAMELLAE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND ONLY IN PERIPHERAL NERVOUS SYSTEM
 CC SCHWANN CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN P0 PROTEIN FAMILY.
 CC -----
 CC PIR: A61087; A61087.
 CC HSSP: P06907; INEU.
 CC InterPro: IPR003596; Ig_MHC.
 CC InterPro: IPR003596; Ig_V.
 CC InterPro: IPR000920; Myelin_P0.
 CC InterPro: IPR000477; Ig_1.
 CC PRINTS: PR00213; MYELINP0.
 CC SMART: SM00406; IGV; 1.
 CC PROSITE: PS00568; MYELIN_P0; 1.
 CC Myelin; Structural protein; Glycoprotein; Transmembrane;
 KW Phosphorylation; Immunoglobulin domain; Signal.
 KM SIGNAL 1 29
 FT CHAIN 30 249 MYELIN P0 PROTEIN.
 FT DOMAIN 30 153 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 154 179 POTENTIAL.
 FT DOMAIN 180 249 CYTOPLASMIC.
 FT DISULFID 50 127 POTENTIAL.
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 249 AA; 27466 MW; FBD14801FF8A08FB CRC64;
 Query Match 7.7%; Score 110.5; DB 1; Length 249;
 Best Local Similarity 29.8%; Pred. No. 0.0046; Indels 19; Gaps 6;
 Matches 39; Conservative 23; Mismatches 50;
 QY 2 GRLLALVVGALVSSACG-----CVDSTETAVVGMTEFKILCISCRSEETVAETFE- 56
 DB 9 GRLLALLVVG--LLSASGSPPTLAHYTPRE-VYGVGSHVTLSC---SFWSEWISD 61
 QY 57 ----WTFPRQKTEEFVKILRYENEVLQLEDEFEGRVWNGSRGTDL--ODLSIFITN 112
 DB 62 ISYWHFOAESRPSISIFHYGKQPIYDVGSFKEMEVGNPRK---DGSIVLHND 118
 QY 113 YNHSGDYECV 123
 DB 119 YTDNGTFTCDV 129
 RESULT 10
 MYPO_MOUSE STANDARD; PRT; 248 AA.
 AC P27573;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
 protein) (MPP).
 GN MPZ OR P0.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RESULT 12
 ID MYPO HUMAN STANDARD; PRT; 248 AA.
 AC P25169; O16072;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
 DE protein) (MFP).
 GN MPZ.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92062068; PubMed=1719967;
 RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
 RA Uyemura K.;
 RT "Isolation and sequence determination of cDNA encoding the major
 RT structural protein of human peripheral myelin."
 RL Biochem. Biophys. Res. Commun. 180:515-518(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT CMT-1B HIS-98.
 RX TISSUE=Spinal cord;
 RX MEDLINE=93356807; PubMed=7688964;
 RA Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.;
 RT "Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
 RT type 1.";
 RL Biochem. Biophys. Res. Commun. 194:1317-1322(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94154677; PubMed=7509228;
 RA Pham-Dinh D., Foubil Y., Blanquet F., Mattei M.-G., Roedel N.,
 RA Latour P., Chazot G., Vandenbergh A., Dautigny A.;
 RT "The major peripheral myelin protein zero gene: structure and
 RT localization in the cluster of P0 gamma receptor genes on human
 RT chromosome 1q21.3-q23."
 RL Hum. Mol. Genet. 2:2051-2054(1993).
 RN [4]
 RP REVIEW ON CMT-1B VARIANTS.
 RX MEDLINE=95282670; PubMed=7762451;
 RA Roa B.B., Lupski J.R.;
 RT "Molecular genetics of Charcot-Marie-Tooth neuropathy."
 RL Adv. Hum. Genet. 22:117-152(1994).
 RN [5]
 RP REVIEW ON CMT-1B VARIANTS.
 RX MEDLINE=94302675; PubMed=7518101;
 RA Patel P.I., Lupski J.R.;
 RT "Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
 RT inherited disease."
 RL Trends Genet. 10:128-133(1994).
 RN [6]
 RP REVIEW ON CMT-1B AND DSS VARIANTS.
 RX MEDLINE=99103460; PubMed=9888385;
 RA Nelis E., Hautes N., van Broeckhoven C.;
 RT "Mutations in the peripheral myelin genes and associated genes in
 RT inherited peripheral neuropathies."
 RL Hum. Mutat. 13:11-28(1999).
 RN [7]
 RP VARIANT CMT-1B MET-30.
 RX MEDLINE=94061030; PubMed=7694726;
 RA Hayasaka K., Takada G., Tonasescu V.V.;
 RT "Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
 RT type 1B."
 RL Hum. Mol. Genet. 2:1369-1372(1993).
 RN [8]
 RP VARIANT CMT-1B CYS-82.
 RX MEDLINE=94083941; PubMed=7505151;
 RA Himoro M., Yoshikawa H., Matsui T., Mitsui Y., Takahashi M.,
 RA Kaido M., Nishimura T., Sawaishi Y., Takada G., Hayasaka K.;

RT "New mutation of the myelin P0 gene in a pedigree of
 RT Charcot-Marie-Tooth neuropathy 1.";
 RL Biochem. Mol. Biol. Int. 31:169-173(1993).
 RN [9]
 RP VARIANTS CMT-1B GLU-90 AND GLU-96.
 RX MEDLINE=94035113; PubMed=7693129.
 RA Hayasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N.,
 RA Baid T.D., Connolly P.W., Chance P.F.;
 RT "Charcot-Marie-Tooth neuropathy type 1B is associated with mutations
 RT of the myelin P0 gene."
 RL Nat. Genet. 5:31-34(1993).
 RN [10]
 RP VARIANT CMT-1B SER-63 DEL.
 RX MEDLINE=94035114; PubMed=7693130.
 RA Valkens T., Bolhuis P.A., Wolterman R.A., Kemp S., Te Nijenhuis S.,
 RA Valentijn L.J., Hensels G.W., Jennekens F.G., de Visser M.,
 RA Hoogendijk J.E., Baas F.;
 RT "Deletion of the serine 34 codon from the major peripheral myelin
 RT protein P0 gene in Charcot-Marie-Tooth disease type 1B."
 RL Nat. Genet. 5:35-39(1993).
 RN [11]
 RP VARIANT CMT-1B GLU-96.
 RX MEDLINE=94068501; PubMed=7504284;
 RA Su Y., Brooke D.G., Li L., Lepercq J., Trofatter J.A., Ravetch J.V.,
 RA Lebo R.V.;
 RT "Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B
 RT patients."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10856-10860(1993).
 RN [12]
 RP VARIANTS DSS CYS-63 AND ARG-167.
 RX MEDLINE=94100981; PubMed=7506095;
 RA Hayasaka K., Himoro M., Sawaishi Y., Nanao K., Takahashi T.,
 RA Takada G., Nicholson G.A., Olivier R.A., Tachi N.;
 RT "De novo mutation of the myelin P0 gene in Dejerine-Sottas disease
 RT (hereditary motor and sensory neuropathy type III)."
 RL Nat. Genet. 5:266-268(1993).
 RN [13]
 RP VARIANTS CMT-1B LEU-78 AND ASN-134.
 RX MEDLINE=95080774; PubMed=7527371;
 RA Nelis E., Timmerman V., de Jonghe P., Vandenbergh A., Pham-Dinh D.,
 RA Dautigny A., Martin J.J., van Broeckhoven C.;
 RT "Rapid screening of myelin genes in CMT1 patients by SSCP analysis:
 RT identification of new mutations and polymorphisms in the P0 gene."
 RL Hum. Genet. 94:653-657(1994).
 RN [14]
 RP VARIANT CMT-1B PHE-63.
 RX MEDLINE=96432254; PubMed=8835320;
 RA Blanquet F., Pham-Dinh D., Dautigny A., Latour P.,
 RA Bonneau C., Corbillion E., Chazot G., Vandenbergh A.;
 RT "Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63
 RT codon in the major peripheral myelin glycoprotein P0 gene."
 RL Clin. Genet. 48:281-283(1995).
 RN [15]
 RP VARIANTS CMT-1B LEU-78 AND CYS-101.
 RX MEDLINE=96055517; PubMed=7550231;
 RA Latour P., Blanquet F., Nelis E., Bonnebouche C., Chapon F.,
 RA Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G.,
 RA Boucherat M., van Broeckhoven C., Vandenbergh A.;
 RT "Mutations in the myelin protein zero gene associated with
 RT Charcot-Marie-Tooth disease type 1B."
 RL Hum. Mutat. 6:50-54(1995).
 RN [16]
 RP VARIANT DSS PHE-64 DEL.
 RX MEDLINE=96212920; PubMed=8630052;
 RA Ikegami T., Nicholson G., Ikeda H., Ishida A., Johnston H., Wise G.,
 RA Olivier R., Hayasaka K.;
 RT "A novel homozygous mutation of the myelin P0 gene producing
 RT Dejerine-Sottas disease (hereditary motor and sensory neuropathy
 RT type III)."
 RL Biochem. Biophys. Res. Commun. 222:107-110(1996).
 RN [17]
 RP VARIANTS CMT-1B THR-135 AND SER-137.
 RX MEDLINE=96263736; PubMed=8664899;

RA Roa B.B., Warner L.E., Garcia C.A., Russo D., Lovelace R.,
 RA Chance P.F., Lupski J.R.,
 RT "Myelin protein zero (MPZ) gene mutations in nonduplication type 1
 RT Charcot-Marie-Tooth disease.";
 RL Hum. Mutat. 7:36-45(1996).
 RN [18]
 RP VARIANT CMT-1B SER-122.
 RX MEDLINE=97001227; PubMed=8844219;
 RA Blauquet-Grosjean P., Pham-Dinh D., Dautigny A., Latour P.,
 RA Bonnebouche C., Diraison P., Chapon F., Chazot G., Vandenberghe A.,
 RT "Charcot-Marie-Tooth type 1B neuropathy: a mutation at the single
 RT glycosylation site in the major peripheral myelin glycoprotein Po.";
 RL Hum. Mutat. 8:185-186(1996).
 RN [19]
 RP VARIANTS CMT-1B/DSS I-34; C-98; H-98; R-130 AND L-135.
 RX MEDLINE=96304049; PubMed=8797476;
 RA Gabreels-Festen A.A.W.M., Hoogendijk J.E., Meijerink P.H.,
 RA Gabreels F.J.M., Bolhuis P.A., van Beersum S., Kilians T., Nelis E.,
 RA Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,
 RA Marianen B.C.,
 RT "Two divergent types of nerve pathology in patients with different PO
 RT mutations in Charcot-Marie-Tooth disease.";
 RL Neurology 47:761-765(1996).
 RN [20]
 RP VARIANTS CMT-1B CYS-98 AND SER-98, AND VARIANT DSS CYS-98.
 RX MEDLINE=96413554; PubMed=8816708;
 RA Warner L.E., Hilz M.J., Appel S.H., Killian J.M., Kolodry E.H.,
 RA Karpelt G., Carpenter S., Walters G.V., Wheeler C., Wilt D.,
 RA Bodeli A., Nelis E., van Broeckhoven C., Lupski J.R.,
 RT "Clinical phenotypes of different MPZ (P0) mutations may include
 RT Charcot-Marie-Tooth type 1B, Dejerine-Sottas, and congenital
 RT hypomyelination.";
 RL Neuron 17:451-460(1996).
 RN [21]
 RP VARIANT CMT-1B GLU-93.
 RX MEDLINE=97360207; PubMed=9217235;
 RA Ikegami T., Ikeda H., Mitsui T., Hayasaka K., Ishii S.,
 RT "Novel mutation of the myelin Po gene in a pedigree with Charcot-
 RT Marie-Tooth disease type 1B.";
 RL Am. J. Med. Genet. 71:246-248(1997).
 RN [22]
 RP VARIANT CMT-1B LEU-78, AND VARIANT DSS CYS-98.
 RX MEDLINE=9731335; PubMed=9187667;
 RA Bort S., Nelis E., Timmerman V., Sevilla T., Cruz-Martinez A.,
 RA Martinez F., Millan J.M., Arpa J., Vilchez J.J., Prieto F.,
 RA van Broeckhoven C., Palau F.,
 RT "Mutation analysis of the MPZ, PMP22 and Cx32 genes in patients of
 RT Spanish ancestry with Charcot-Marie-Tooth disease and hereditary
 RT neuropathy with liability to pressure palsies.";
 RL Hum. Genet. 99:746-754(1997).
 RN [23]
 RP VARIANT CMT-1B ARG-81.
 RX MEDLINE=9714190; PubMed=8990016;
 RA Sorour E., Macmillan J., Upadhyaya M.,
 RT "Novel mutation of the myelin P0 gene in a CMT1B family.";
 RL Hum. Mutat. 9:74-77(1997).
 RN [24]
 RP VARIANTS DSS THR-114; HIS-116 AND ASN-128.
 Query Match 6.8%; Score 98.5; DB 1; Length 248;
 Best Local Similarity 26.4%; Pred. No. 0.06;
 Matches 32; Conservative 23; Mismatches 61; Indels 5; Gaps 3;

DB 129 V 129
 RESULT 13
 ID MK01 XENILA STANDARD; PRT; 361 AA.
 AC P26696;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Mitogen-activated protein kinase (EC 2.7.1.-) (Myelin XP42 protein
 DE kinase) (Myelin basic protein kinase) (MBP kinase) (M phase MAP
 DE kinase).
 GN XP42 OR MPKL.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=91203872; PubMed=1708093;
 RA Posada J., Sanghera J., Pelech S., Aebersold R., Cooper J.A.,
 RT "Tyrosine phosphorylation and activation of homologous protein
 RT kinases during oocyte maturation and mitogenic activation of
 RT fibroblasts.";
 RL Mol. Cell. Biol. 11:2517-2528(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Oocyte;
 RX MEDLINE=91330892; PubMed=1714387;
 RA Gotch Y., Moriyama K., Matsuda S., Okumura E., Kishimoto T.,
 RA Kawasaki H., Suzuki K., Yahara I., Sakai H., Nishida E.,
 RT "Xenopus M phase MAP kinase: isolation of its cDNA and activation by
 RT MPF.";
 RL EMBO J. 10:2661-2668(1991).
 RN [3]
 RP PHOSPHORYLATION SITES, AND MUTAGENESIS.
 RX MEDLINE=92205337; PubMed=1313186;
 RA Posada J., Cooper J.A.,
 RT "Requirements for phosphorylation of MAP kinase during meiosis in
 RT xenopus oocytes.";
 RL Science 255:212-215(1992).
 CC -1- FUNCTION: PHOSPHORYLATES MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2).
 CC MYELIN BASIC PROTEIN (MBP), AND ELK-1; MAY PROMOTE ENTRY IN THE
 CC CELL CYCLE. ACTIVATED BY M PHASE PROMOTING FACTOR (MPF).
 CC -1- ENZYME REGULATION: ACTIVATED WITH TYROSINE PHOSPHORYLATION DURING
 CC THE M PHASE OF THE MEIOTIC CELL CYCLE.
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN THE CENTRAL NERVOUS SYSTEM,
 CC KIDNEYS, LIVER, INTESTINE AND THE HEMATOPOIETIC SYSTEM. ALSO FOUND
 CC IN HEART, MUSCLE, PANCREAS, AND LUNG.
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED IN THE EARLY OCYTE AND IS
 CC MAINTAINED AT A CONSTANT LEVEL DURING EMBRYOGENESIS. ITS
 CC LEVEL DECLINES AT THE MID-BLASTULA TRANSITION.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sb.ch).
 CC -----
 DR EMBL: M60977; AAA50002.1; -
 DR EMBL: X59813; CA42482.1; -
 DR PIR: S16597; S16597.
 DR PIR: A39754; A39754.
 DR HSSP: P27703; 1ERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.

InterPro: IPR002290; Ser thr_kinase.
 DR Pfam: PF00069; kinase: 1.
 DR Prodom: PD000001; Euk_kinase: 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; 1.
 DR PROSITE: PS01017; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS01018; PROTEIN KINASE ST; 1.
 KM Transferase: Serine/threonine-protein kinase; ATP-binding; Cell cycle; Phosphorylation.
 FT DOMAIN 2 6
 FT NE_BIND 28 316
 FT BINDING 34 42
 FT ACT_SITE 57 57
 FT MOD_RES 152 152
 FT MOD_RES 188 188
 FT MOD_RES 190 190
 FT MUTAGEN 57 57
 FT MUTAGEN 86 86
 FT MUTAGEN 188 188
 FT MUTAGEN 190 190
 FT CONFLICT 5 5
 FT CONFLICT 7 7
 FT CONFLICT 29 29
 FT CONFLICT 32 32
 FT CONFLICT 47 47
 FT CONFLICT 49 49
 SQ SEQUENCE 361 AA; 41292 MW; 663CBDE57EC26F9C CRC64;
 Query Match
 Best Local Similarity 20.1%; Score 98; DB 1; Length 361;
 Matches 56; Conservative 49; Mismatches 80; Indels 94; Gaps 16;
 QY 29 EAVYGMFKILC-----ISCKRSETNAETFTMTFROKGTETFKII---RYE----- 74
 DB 36 EGAVGVCASHCNINKRAIKISPEHOTYCRLRE-----IKILRFHEHTIIGI 89
 QY 75 NEVLQLEDEDERFGRVYVWNGSRGTQDLQDISIFITVYVNHSGDYCH-VYRLFFENYE 133
 DB 90 NDIIRAPTEIQMDVYI-----VQDLMETDLYKLTQKTHLSNDHCYFLYQILRLAKYI 143
 QY 134 HNTSVYKK-----IHIEVVDKSGSAGACPTVTHRRARWRDQAVDRGTWC 181
 DB 144 HSNANVLRDIPKPSNLLNTCTDILKICDFGLARVADP---DH--DHGFLT 188
 QY 182 AWPANR-----PQORAGEGSSPSCPQLW-----PLFLSSPRGQSPVPHR 224
 DB 189 EYVATRWYARPELIMNSKGYTS--IDIMSVGCIAMLSNRPIF-----PKKH- 235
 QY 225 RSGYRQLCHLCMTSG-----RCLLSLSQR-VVLGLP 256
 DB 236 ---YLDQLNHIIIGLISPSQEDINCTIINKARYVLLSLP 271
 RESULT 14
 BY55_HUMAN STANDARD; PRT; 181 AA.
 ID BY55_HUMAN
 AC 095971;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CD160 antigen precursor (Natural killer cell receptor BY55).
 GN CD160 OR BY55.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98414268; PubMed=9743336;
 RA Anumathan A., Bensussan A., Bounsell L., Christ A.D., Blumberg R.S.,
 RA Voss S.D., Patel A.T., Robertson M.J., Nadler L.M., Freeman G.J.,
 RT "Cloning of BY55, a novel Ig superfamily member expressed on NK cells,

CTL, and intestinal intraepithelial lymphocytes."; RT
 J. Immunol. 161:2780-2790(1998).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=99138795; PubMed=9973372;
 RA Agrawal S., Maruet J., Freeman G.J., Tawab A., Boueiller P.L.,
 RA Roth P., Bolton W., Oss G., Bounsell L., Bensussan A.,
 RT "cutting edge: MHC class I triggering by a novel cell surface ligand
 RT costimulates proliferation of activated human T cells."; RT
 J. Immunol. 162:1223-1226(1999).
 RL -1- FUNCTION: Receptor showing broad specificity for both classical
 CC and nonclassical MHC class I molecules.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, peripheral blood, and
 CC small intestine. Expression is restricted to functional NK and T
 CC cytotoxic lymphocytes.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 1:72-73(2000).
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/160590458.g.htm".
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF060981; AAC72302.1; -
 DR MIM; 604463; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00410; IG_Like; 1.
 KW Receptor; GPI-anchor; Glycoprotein; Signal; Immunoglobulin domain;
 FT STGNAL 1 26
 FT CHAIN 27 159
 FT PROPEP 160 181
 FT DOMAIN 37 119
 FT DISULFID 44 112
 FT DISULFID 61 68
 FT CARBOHYD 28 28
 FT CARBOHYD 137 137
 FT LIPID 159 159
 SQ SEQUENCE 181 AA; 19810 MW; EF0B981AC7478BD CRC64;
 Query Match
 Best Local Similarity 22.6%; Score 94; DB 1; Length 181;
 Matches 36; Conservative 28; Mismatches 57; Indels 38; Gaps 7;
 QY 6 ALVGAALVSACGGCVENDETEAVYGMFKILCISCKRSETNAETFTMTFROK--- 62
 DB 11 ALAILAIVDIQSGGGINITS--SASQEGTRIMLICVWKKKE--AEGVVFLCKDRSD 67
 QY 63 -GTDEFYKILRYNEVLQLEDEDERFGRVYVWNGSRGTQDLQDISF--ITVYVNHSGDY 120
 DB 68 CSPETSIKQRLKRD-----PEIDVGISISQMLMTTISQVPLHSQGTQ 111
 QY 121 C-----HYRLFFENYEHN-TSYVKIHI 145
 DB 112 CCARSKSGIRLQGHFFSILFTGTGNYTGLKQROHLE 150
 RESULT 15
 MK01_MOUSE STANDARD; PRT; 358 AA.
 ID MK01_MOUSE
 AC P27703;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Mitogen-activated protein kinase 1 (EC 2.7.1.1-) (Extracellular signal-
DE regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP
DE kinase 2) (MAPK 2) (P42-MAPK) (ERK1).
DE MAPK1 OR PRK1 OR ERK2 OR MAPK.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Homo; STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=91235302; PubMed=2032220;
RA Boulton T.G., Nye S.H., Robbins D.J., Ip N.Y., Radziejewska E.,
RA Morganbeaser S.D., Delinho R.A., Panayotatos N., Cobb M.H.,
RA Yancopoulos G.D.;
RT "ERKs: a family of protein-serine/threonine kinases that are
RT activated and tyrosine phosphorylated in response to insulin and
RT NGF";
RL Cell 65:663-675 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=Swiss; TISSUE=Fibroblast;
RX MEDLINE=91305126; PubMed=1649458;
RA Her J.-H., Wu J., Rall T.B., Sturgill T.W., Weber M.J.;
RT "Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by
RT tyrosine phosphorylation";
RL Nucleic Acids Res. 19:3743-3743 (1991).
RN [3]
RP SEQUENCE OF 151-189 FROM N.A.
RC SPECIES=Mouse; STRAIN=CBA; TISSUE=Bone marrow;
RX MEDLINE=91859941; PubMed=844335;
RA Ershler M.A., Nagotekaya T.V., Visser J.W.M., Belyavsky A.V.;
RT "Novel CDC2-related protein kinases produced in murine hematopoietic
RT stem cells";
RL Gene 124:305-306 (1993).
RN [4]
RP PHOSPHORYLATION SITES OF THR-183 AND TYR-185, AND PARTIAL SEQUENCE.
RC SPECIES=Mouse;
RX MEDLINE=91184134; PubMed=1849075;
RA Payne D.W., Rosemond A.J., Martino P., Erickson A.K., Her J.-H.,
RA Shabanowitz J., Hunt D.F., Weber M.J., Sturgill T.W.;
RT "Identification of the regulatory phosphorylation sites in
RT pp42/mitogen-activated protein kinase (MAP kinase)";
RL EMBO J. 10:885-892 (1991).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES=Rat;
RX MEDLINE=94150699; PubMed=8107865;
RA Zhang F., Strand A., Robbins D., Cobb M.H., Goldsmith E.J.;
RT "Atomic structure of the MAP kinase ERK2 at 2.3-A resolution.";
RL Nature 367:704-710 (1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC SPECIES=Rat;
RX MEDLINE=97443349; PubMed=9298898;
RA Canagarajah B.J., Khokhachev A., Cobb M.H., Goldsmith E.J.;
RT "Activation mechanism of the MAP kinase ERK2 by dual
RT phosphorylation";
RL Cell 90:859-869 (1997).
RN [7]
RP AUTOPHOSPHORYLATION.
RC SPECIES=Rat;
RX MEDLINE=91296777; PubMed=1712480;
RA Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Panayotatos N.,
RA Radziejewska E., Erickson L., Brattlien R.L., Cobb M.H., Krebs E.G.;
RT "Microtubule-associated protein 2 kinases, ERK1 and ERK2, undergo
RT autophosphorylation on both tyrosine and threonine residues:
RT implications for their mechanism of activation";
RL Proc. Natl. Acad. Sci. U.S.A. 88:6142-6146 (1991).
CC -!- FUNCTION: PHOSPHORYLATES MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2).
CC MYELIN BASIC PROTEIN (MBP), AND ELK-1; MAY PROMOTE ENTRY IN THE
CC CELL CYCLE.

CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION ON TYROSINE AND
CC THREONINE IN RESPONSE TO INSULIN AND NGF. BOTH PHOSPHORYLATIONS
CC ARE REQUIRED FOR ACTIVITY.
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS WITHIN THE NERVOUS SYSTEM,
CC EXPRESSED IN DIFFERENT TISSUES, MOSTLY IN MUSCLE, THYMUS, AND
CC HEART.
CC -!- DEVELOPMENTAL STAGE: INCREASED EXPRESSION DURING DEVELOPMENT.
CC -!- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES,
CC WHICH CORRELATES WITH A SLOW AND LOW LEVEL OF AUTOACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: M64300; AAA41124.1; -;
DR EMBL: X58712; CAA41548.1; -;
DR EMBL: D10939; BAA01733.1; -;
DR PIR: S16444; S16444.
DR PIR: A40033; A40033.
DR PDB: 1ERK; 15-MAY-97.
DR PDB: 2ERK; 01-JUL-98.
DR PDB: 1GOL; 12-MAR-97.
DR MGD: MGI:134658; Mapk1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
KW Phosphorylation; 3D-structure.
FT DOMAIN 2 7
FT NP_BIND 23 311 POLY-ALA.
FT BINDING 29 37 PROTEIN KINASE.
FT ACT_SITE 52 52 ATP.
FT ACT_SITE 147 147
FT MOD_RES 183 183
FT MOD_RES 185 185
SQ SEQUENCE 358 AA; 41275 MW; 3B8CF22471EDBA08 CRC64;
Query Match 6.5%; Score 94; DB 1; Length 358;
Best Local Similarity 20.1%; Pred. No. 0.24; Matches 102; Gaps 17;
Matches 57; Conservative 49; Mismatches 75; Indels 102; Gaps 17;
QY 29 EAYGMPFKILC-----ISCKRSETNAETFTMTFRKGTBEVFKIL---RYE 74
DB 31 EGAIGM-----VCSAYVDLNVKRAVIAIKISPEFGTYCQRLRE-----IKILLRRHN 80
QY 75 -----NEVLQLEDERFEGRYVWNGSRGTQDLQDLSIFITNVYNSGDYECR-VRLLEF 129
DB 81 IIGINDIRAPFTIEQMDOYI-----VQDLMEITDLYKLLKTOHLNDHICFPLYOILNG 134
QY 130 ENYENANISVYVK-----IHIEVVDKESGAGCFYVTHRRARRDRMQAVDRT 177
DB 135 LKYHSANVAVLRDLKPSNLLNTTCDIKCDFGLARVADP---DH-----DHT 179
QY 178 GWLCAMPANR-----POORAEGEGSSPSCPQLW-----PLFLSPRRQSNMP 220
DB 180 GFLREYVATRYRRAPEIMANSKGYTKS-IDIVSGCILAEMLSNRPIF-----P 227
QY 221 VPHRRSGYRQLCHLCMTSG-----RCLLSLSQR-VVGLP 256
DB 228 GKG-----YLDQNLHILGILSPSOEDLNCIINLKARVYLLSLP 266

Fri Jan 31 07:51:23 2003

us-09-875-456a-14.rsp

Page 12

Search completed: January 29, 2003, 13:28:33
Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 29, 2003, 13:26:52 ; Search time 33 Seconds
(without alignments)
1673.352 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444
Sequence: 1 MGRLLALVGAALVSSACGG.....QRVGLPGIIRCVSRGVV 268

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21: *
1: sp archaea: *
2: sp bacteria: *
3: sp fungi: *
4: sp human: *
5: sp invertebrate: *
6: sp mammal: *
7: sp mhc: *
8: sp organelle: *
9: sp phage: *
10: sp plant: *
11: sp rodent: *
12: sp virus: *
13: sp vertebrate: *
14: sp unclassified: *
15: sp virus: *
16: sp bacteriophage: *
17: sp archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	817	56.6	273	11 090XU3	Q9GXU3 ratius norv
2	620	42.9	185	4 Q8WU42	Q8WU42 homo sapien
3	259.5	18.0	215	11 0912B9	Q912B9 mus musculu
4	258.5	17.9	230	4 Q9ULR2	Q9ULR2 homo sapien
5	257.5	17.8	215	11 09JK00	Q9JK00 ratius norv
6	114.5	7.9	209	4 Q9NYK4	Q9NYK4 homo sapien
7	114.5	7.9	269	4 Q9S297	Q9S297 homo sapien
8	109	7.5	183	4 Q9UEU6	Q9UEU6 homo sapien
9	109	7.5	243	4 Q9UEU4	Q9UEU4 homo sapien
10	108.5	7.5	215	11 091W14	Q91W14 mus musculu
11	103.5	7.2	203	4 Q9EMJ0	Q9EMJ0 homo sapien
12	102	7.1	368	13 Q8WU66	Q8WU66 gallus gall
13	101.5	7.0	202	13 Q91406	Q91406 salmo sp. 1
14	98.5	6.8	251	4 Q14902	Q14902 homo sapien
15	98.5	6.8	251	4 Q9BR67	Q9BR67 homo sapien
16	98	6.8	412	4 Q96PW2	Q96PW2 homo sapien

17	96.5	6.7	280	13 Q8WU1	Q8WU1 ictalurus p
18	96.5	6.7	280	13 Q8WU1	Q8WU1 ictalurus p
19	96	6.6	567	4 Q96KV6	Q96KV6 homo sapien
20	92.5	6.4	1099	10 Q9XFK8	Q9XFK8 zea mays lm
21	92	6.4	333	12 Q9QC01	Q9QC01 simian cyto
22	92	6.4	5198	5 Q76518	Q76518 caenorhabdi
23	91.5	6.3	369	13 Q9DGR5	Q9DGR5 brachydanio
24	91.5	6.3	4292	4 Q15141	Q15141 homo sapien
25	91.5	6.3	4302	4 Q15140	Q15140 homo sapien
26	90	6.2	225	4 Q92677	Q92677 homo sapien
27	89.5	6.2	438	11 Q9JUB7	Q9JUB7 mus musculu
28	89.5	6.2	510	11 Q9JUB8	Q9JUB8 mus musculu
29	89.5	6.2	549	11 Q9JUB9	Q9JUB9 mus musculu
30	89	6.2	128	13 Q90562	Q90562 ginglymosto
31	89	6.2	549	11 Q9D006	Q9D006 mus musculu
32	87.5	6.1	336	4 Q8WV5	Q8WV5 homo sapien
33	87.5	6.1	523	4 Q00480	Q00480 homo sapien
34	87.5	6.1	1200	10 Q8W50	Q8W50 oryza sativ
35	85.5	5.9	1327	4 Q15070	Q15070 homo sapien
36	85	5.9	759	4 Q96K57	Q96K57 homo sapien
37	85	5.9	777	4 Q9HBP4	Q9HBP4 homo sapien
38	85	5.9	816	4 Q9HC13	Q9HC13 homo sapien
39	84.5	5.9	291	11 Q35558	Q35558 mus musculu
40	84	5.8	458	2 Q932V1	Q932V1 rhodococcus
41	84	5.8	698	2 Q8SYE9	Q8SYE9 drosophila
42	84	5.8	948	2 Q30483	Q30483 streptomyce
43	83.5	5.8	217	5 Q9VQ95	Q9VQ95 drosophila
44	83.5	5.8	268	13 Q90524	Q90524 ginglymosto
45	83.5	5.8	357	12 Q91TU3	Q91TU3 tupata herp

ALIGNMENTS

RESULT 1

ID	Q9GXU3	PRELIMINARY:	PRT:	273 AA.
AC	Q9GXU3;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Voltage-gated sodium channel subunit beta1-A.			
GN	SCN1B.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20092877; PubMed=10625649;			
RA	Kazen-Gillespie K.A., Ragsdale D.S., D'Andrea M.R., Mattei L.N.,			
RA	"Cloning, localization, and functional expression of sodium channel			
RT	beta1A subunits."			
RL	J. Biol. Chem. 275:1079-1088 (2000).			
DR	EMBL; AF182949; AAF25186.1; -			
DR	InterPro; IPR003600; IG_1like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	Pfam; PF00047; IG_1like; 1.			
KW	SMART; SM00640; IG_1like; 1.			
SQ	SEQUENCE 273 AA; 31063 MW; 156A31899A906849 CRC64;			

Query Match 56.6%; Score 817; DB 11; Length 273;
Best local Similarity 69.2%; Pred. No. 6.6e-73;
Matches 173; Conservative 14; Mismatches 39; Indels 24; Gaps 7;

Qy	1	MGRLLALVGAALVSSACGGCEVDSETEVYGMETKILICISKRKRSRTAEFTETPR 60
Db	1	MGRLLALVGAALVSSACGGCEVDSETEVYGMETKILICISKRKRSRTAEFTETPR 60
Qy	61	QKGEFEEVKILRYENEYLOLEEDERPEGRVVMNGSRGTQDLOLSIFITVTYVNSGDYE 120

Db 61 QKTEEPVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLDSIFITVTVNHSQDY 120
 QY 121 CHVRLFFPENYEHTSVVKKIHLEVDKSGSACPTTYHRRARMDRQAVDRIGWL 180
 Db 121 CHVRLFFPENYEHTSVVKKIHLEVDKSGS-----LVTLWQARMDRKEEDRL--- 172
 QY 181 CAMPANPO--QRAEGSSSPSCPLQPLWPLFLSSPRQO--SMPVPHRRSGYRTQLC---H 234
 Db 173 ---VSHRGQLPRSHRGQDTFVIVLTSAL---QHTGQITPTPPPPNG---WCTGLH 222
 QY 235 LCMNTSGRCL 244
 Db 223 SCCVTSIDGCI 232

RESULT 2

Q8WU42 PRELIMINARY; PRT; 185 AA.

AC Q8WU42; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 OS Hypothetical 21.5 kDa protein.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RU Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021266; AAH21266.1; -
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 KM Hypothetical protein.
 SQ SEQUENCE 185 AA; 21497 MW; CFE5B8510DC59800 CRC64;

Query Match

Best Local Similarity 42.9%; Score 620; DB 4; Length 185;
 Matches 117; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 34 MTFKILICISCKRSENAETFTETPROKGTETPEVKILRYENEVLQLEDERFEGRVVWN 93
 Db 1 MTFKILICISCKRSENAETFTETPROKGTETPEVKILRYENEVLQLEDERFEGRVVWN 60
 QY 94 GSRGTQDLQDLISFITVTVNHSQDYECYVRLFFPENYEHTSVVKKIHLEVDKSGS 153
 Db 61 GSRGTQDLQDLISFITVTVNHSQDYECYVRLFFPENYEHTSVVKKIHLEVDKSGS 120
 QY 154 AA 155
 Db 121 MA 122

RESULT 3

Q91Z99 PRELIMINARY; PRT; 215 AA.

AC Q91Z99; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 OS Brain and heart sodium channel beta 3 subunit.
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen C.; Avery C.; Kazen-Gillespie K.; Isom L.D.;
 RT "Mouse brain and heart beta 3 sodium channel cDNA";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY049036; AAL07512.1; -

DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 KW Ionic channel.
 SQ SEQUENCE 215 AA; 24771 MW; 0E9EB4704178A42C CRC64;

Query Match

Best Local Similarity 18.0%; Score 259.5; DB 11; Length 215;
 Matches 59; Conservative 20; Mismatches 46; Indels 7; Gaps 4;

QY 21 CVEVDSETEAVYGMTFKILICISCKRSENAETFTETPROKGTETPEVKILRYENEVLQ 80
 Db 26 CVEVDSETEAVYGMTFKILICISCKRSENAETFTETPROKGTETPEVKILRYENEVLQ 84
 QY 81 EEDERFEGRVVWNGSRGTQDLDSIFITVTVNHSQDYECYVRLFFPENYEHTSVVK 140
 Db 85 ESP--FOGRLQWNGS---KDLQDVSITVTVNHSQDYECYVRLFFPENYEHTSVVK 139
 QY 141 KIHIEVDK-GE 151
 Db 140 LIPKVTPEAGE 151

RESULT 4

Q9ULR2 PRELIMINARY; PRT; 230 AA.

AC Q9ULR2; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN KIAA1158 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hirotsawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the Genemark analysis
 from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 DR EMBL; AB032984; BAA86472.1; -
 DR HSSP; P06907; INEU
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IG_1.
 FT NON TER 1 1
 SQ SEQUENCE 230 AA; 26357 MW; B06D5155SF5F98 CRC64;

Query Match

Best Local Similarity 17.9%; Score 258.5; DB 4; Length 230;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 5 LATVGAALVSSACGCVEDSETEAVYGMTFKILICISCKRSENAETFTETPROKGT 64
 Db 25 LATVGAALVSSACGCVEDSETEAVYGMTFKILICISCKRSENAETFTETPROKGT 84
 QY 65 EEPVKILRYENEVLQLEDERFEGRVVWNGSRGTQDLDSIFITVTVNHSQDYECYV 124
 Db 85 KDFL-IYEYRNGHGVESP--FOGRLQWNGS---KDLQDVSITVTVNHSQDYECYV 138
 QY 125 RLFPEYHNTSVVKKIHLEVDK-GE 151
 Db 139 REFEFAHRPFTKTRILPLRVTPEAGE 166

RESULT 5

Q9UK00 PRELIMINARY; PRT; 215 AA.

AC Q9UK00; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN KIAA1158 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirotsawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the Genemark analysis
 from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 DR EMBL; AB032984; BAA86472.1; -
 DR HSSP; P06907; INEU
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IG_1.
 FT NON TER 1 1
 SQ SEQUENCE 230 AA; 26357 MW; B06D5155SF5F98 CRC64;

DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Voltage-gated sodium channel beta-3 subunit (Sodium channel beta 3 subunit).
 GN SCN3B OR SCN3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN;
 RX MEDLINE=20160948; PubMed=1068874;
 RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K., Plunick R.D., Hughes J., Richardson P.J., Minguich K., Jackson A.P.; "beta3: An additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics."; Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLION;
 RA Ou Y., Curtis R., Lawson D., Gilbride K., Ge P., DiStefano P.S., Silos-Santago I., Caterall W.A., Scheuer T.; "Differential Modulation of Sodium Channel Gating and Persistent Sodium Currents by the beta1, beta2, and beta3 subunits."; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ374339; CAB76838.1; -
 DR EMBL; AJ374339; CAB76838.1; -
 DR HSSP; P06907; INEU.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SMO0409; IG; 1.
 KM Ionic channel.
 SQ SEQUENCE 215 AA; 24799 MW; 056B488F5AE64F CRC64;
 Query Match 17.8%; Score 257.5; DB 11; Length 215;
 Best Local Similarity 44.7%; Pred. No. 1.8e-17;
 Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;
 QY 21 CVDSTSTVYGMTPFKILCTSCRRSETNAETFTWTFKQKTEEVKLRLENVQL 80
 DB 26 CVDSTSTVYGMTPFKILCTSCRRSETNAETFTWTFKQKTEEVKLRLENVQL 84
 QY 81 EEDRPFGRVYVNGSRGKTDQDLSIFITVYVHSGDYCHVYRLLEFNYEHNTSVK 140
 DB 85 ESDP--FGGRLOMNGS--KLDQDVSTVLTNTLNDGLITCNVSRLEPFAHHPFYKTT 139
 QY 141 KIHIEVYDK-GE 151
 DB 140 LIPLRVTEAGE 151
 RESULT 6
 Q9NRY4 PRELIMINARY; PRT; 209 AA.
 AC Q9NRY4;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE P2R1D.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhao R., Zhao Z.J.; "Identification of a Variant Form of P2R Lacking Immuneceptor Tyrosine-Based Inhibitory Motifs."; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF639756; AAF63499.1; -

DR HSSP; P06907; INEU.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR000920; Myelin_PO.
 DR Pfam; PF00047; IG; 1.
 DR PRINTS; PR00213; MYELINPO.
 DR SMART; SMO0406; IG; 1.
 SQ SEQUENCE 209 AA; 22761 MW; 18EC385959C88329 CRC64;
 Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.0028;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
 QY 3 RLIALVGAALVSSACG-CGVEVDSETE--AVYGMTPFKILCTSCRRSETNAETFTWTF 59
 DB 18 RLIALVGAALVSSACG-CGVEVDSETE--AVYGMTPFKILCTSCRRSETNAETFTWTF 76
 QY 60 RQKTEEPFKILRYENYVQLSEDERFGRVYVNGSRGKTDQDLSIFITVYVHSGDY 119
 DB 77 QEGADTVSPFHYSGQVYLGNYPPFKDRISW--AGDLKDKASINLENNQFIHNGTY 133
 QY 120 ECHV 123
 DB 134 ICDV 137
 RESULT 7
 Q95297 PRELIMINARY; PRT; 269 AA.
 AC Q95297;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Protein ZERO related protein (Myelin protein ZERO-like 1).
 GN PZR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99009038; PubMed=9792637;
 RA Zhao Z.J., Zhao R.; "Purification and cloning of PZR, a binding protein and putative physiological substrate of tyrosine phosphatase SHP-2."; J. Biol. Chem. 273:29367-29372(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Xia J., Liu C.-Y., Yu K., Pan Q., Dai H.-P., Tang X.-X.; "Molecular cloning of myelin protein zero like gene."; Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF087020; AAC72231.1; -
 DR EMBL; AF095727; AAF00064.1; -
 DR EMBL; AF092425; AAD55347.1; -
 DR EMBL; AF095726; AAF00083.1; -
 DR EMBL; BC007881; AAF07881.1; -
 DR HSSP; P06907; INEU.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR000920; Myelin_PO.
 DR Pfam; PF00047; IG; 1.
 DR PRINTS; PR00213; MYELINPO.
 DR SMART; SMO0406; IG; 1.
 SQ SEQUENCE 269 AA; 29082 MW; A1B239041E559425 CRC64;
 Query Match 7.9%; Score 114.5; DB 4; Length 269;
 Best Local Similarity 30.6%; Pred. No. 0.0038;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

[illegible]

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RESULT 8
Q9UEI6 PRELIMINARY; PRT; 183 AA.
ID Q9UEI6
AC Q9UEI6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 20.2 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035302; CAA22907.1; --
DR HSSP; P06907; INEU.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR000920; Myelin_P0.
DR Pfam; PF00047; IG; 1.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGV; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 183 AA; 20230 MW; 571F7B7C514E280 CRC64;

Query Match: 7.5%; Score 109; DB 4; Length 183;
Best Local Similarity 30.8%; Pred. No. 0.0083;
Matches 28; Conservative 12; Mismatches 47; Indels 4; Gaps 2

QY 33 GMTFFILCTICSKRRSETNAETETWTFKQGTKEEFKILRYENVALTEDEFEGRVYW 92
DB 25 GFGKLTTC-KFKSTSTTGGLTSVSWSGFQEGADDTVSPFHYSGQGYLLNYPPEKORISM 83
QY 93 NGSRGTKLDLDISTIFTVTYTNHSGDYECV 123
DB 84 --AGDLDRKASINENMQFIHNGTYICDV 111

RESULT 9
Q9UEI4 PRELIMINARY; PRT; 243 AA.
ID Q9UEI4
AC Q9UEI4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 26.6 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035308; CAA22913.1; --
DR HSSP; P06907; INEU.

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DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_v.
DR   InterPro; IPR000920; Myelin_PO.
DR   Pfam; PF00047; IG; 1.
DR   PRINTS; PR0213; MYELINP0.
DR   SMART; SM00406; IGV; 1.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 243 AA; 26551 MW; DF4B85BBBD3C005D CRC64;
Query Match 7.5%; Score 109; DB 4; Length 243;
      Best Local Similarity 30.8%; Pred. No. 0.012;
Matches 28; Conservative 12; Mismatches 47; Indels 4; Gaps 2;

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QY	33	GMFFKILDISCKRRSETNAETFEWTFQKGTBESEVKILRARENVELQLEEDERPEGRVW	92			
DB	25	GGGQKLTCC-KFESYSTTGGTLTSVMSFQPEGADTTVSFFHYSQGQGVYLGNNPPFPKRLISW	83			
QY	93	NGSRGTXDLDLSIFITVTVYNNHSGDYECVH	123			
DB	64	---AGDLDKKASINIEHQFIHNGTYICDV	111			
RESULT 10						
ID	Q91WI4	PRELIMINARY;	PRT; 215 AA.			
AC	Q91WI4;					
DT	01-DEC-2001	(TREMBLrel. 19, Created)				
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)				
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)				
DE	Epithelial V-like antigen.					
GN	EVA.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Salivary Gland;					
RA	Strausberg R.;					
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; BC015076; AAH15076.1; -					
DR	MCD; MGI:1289160; Eva.					
DR	InterPro; IPR003006; IG_MHC.					
DR	Pfam; PF00047; Ig_1.					
SQ	SEQUENCE 215 AA; 24092 MW; FESEB36787CF79C4 CRC64;					
Query Match 7.5%; Score 108.5; DB 11; Length 215;						
Best local similarity 24.7%; Pred. No. 0.011; 78; Indels 37; Gaps						
Matches 47; Conservative 28; Mismatches 78; Indels 37; Gaps						
QY	4	LIALVGAALVSSACGCGVEV--DSETEAVYGMTFKILICICKRRSETNAETFEWTRQ	61			
DB	9	VLPILLSIQTLALCTPEAVEITSGALAAVNGTDVRLKCTFSSFAVPADALTVT--MNRFP	67			
QY	62	K--GTEEEVKILRYENEVLQLEEDERPEGRVWYNNHSGDY	119			
DB	68	KDGGREQF--FYIMDPR--PMGRFPDQVWDG--PERYDVSILMLKQLQFDNGTY	121			
QY	120	ECHVVRLLFFENYEHTNSVVKKIHLEVD-----KGSQAACEFTVT-----	161			
DB	122	TQGV-----KNPDPVDGLVGTIRLSVHTVPSESIYFLAVALGSCALMIIVIVLVL	175			
QY	162	--HRRARWD	169			
DB	176	OHFRKKWAD	185			
RESULT 11						
ID	Q96MJ0	PRELIMINARY;	PRT; 203 AA.			
AC	Q96MJ0;					
DT	01-DEC-2001	(TREMBLrel. 19, Created)				

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE CDNA FLJ32309 fig. clone PROST2002960, highly similar to human
 DE butyrophilin (BTF1) mRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RA Ishibashi T., Kanehori K., Yosida M., Matanabe S., Ishida S., Ono Y.,
 RA Houta T., Hirooka S., Murakawa K., Takiguchi S., Iusano J.,
 RA Matanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Makamori A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isegai T.,
 RT "NEO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AK056871, BAB71298.1, -
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig_1.
 SQ SEQUENCE 203 AA; 22403 MW; 8035D02584E3A47 CRC64;

 Query Match 7.2%; Score 103.5; DB 4; Length 203;
 Best Local Similarity 26.2%; Pred. No. 0.033;
 Matches 62; Conservative 26; Mismatches 78; Indels 71; Gaps 13;

 QY 4 LIALVGAALVSSACGCGVEVDESEAVYGMTFKILCISCRSEETNAE-----TF 54
 DB 15 LILLLSICALVSAQ---VTVGPDPDILAMVGENITLRCCSPENNAEMERWQSQF 70
 QY 55 TENVTPROKGTETEEVKILRYENVALQLEDERFEGRY--VWNSRGTKDLDLSIFTTNT 112
 DB 71 SPAVFVYKGGRE-----RTE-----EQKEEYRGRITTFVSKDSRG-----VALIHNVT 114
 QY 113 YNNSGDEYCHVYLLPFENYEHNTSVYKTHIEVNDKSGSACPTVYTRRARWRDRNQ 172
 DB 115 AEDNGIYQCY-----PQEGRSCEBAI---LHLVV---AGALLHVALLI----- 151
 QY 173 AVDRGTGLCAMPANRPOQRAEGES--SPSCPLQLMP--LFLSSPRGQSMVPFRRSRG 227
 DB 152 -----WHCV-----TLGKASLNLSSPLQSTLTLPFGSPFRIDTLPKMRFGG 193

 RESULT 12
 Q8UMG6
 ID 08UMG6 PRELIMINARY; PRT; 368 AA.
 AC 08UMG6;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Extracellular signal-regulated kinase 2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phaethonidae; Phaethoninae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PINEAL GLAND;
 RA Kasahara T., Higashi C., Okano T., Fukuda Y.,
 RT "Cloning of ERK2 expressed in the chicken pineal gland."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AY033635; AAKS6503.1, -
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; kinase; 1.
 DR ProDom: PD000001; Euk_kinase; 1.

DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYKC; 1.
 DR PROSITE; PS01351; MAPK; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
 KM Kinase.
 SQ SEQUENCE 368 AA; 41942 MW; A6F3A3D27C6C9A44 CRC64;

 Query Match 7.1%; Score 102; DB 13; Length 368;
 Best Local Similarity 20.4%; Pred. No. 0.098;
 Matches 66; Conservative 52; Mismatches 87; Indels 118; Gaps 19;

 QY 5 LALVVGALV--SSACGCGVEVDESEAVYGMTFKILC-----EAVYGMTFKILC----- 40
 DB 1 MAVAAGAAAGGSAAGGPEWVGQVFGVGRYTNLSYIGGAYGM---VCSAYDVNK 56
 QY 41 --ISCRSEETNAETFTETPROKGTETEEVKIL--RYE-----NEVLQLEDERFEGRY 90
 DB 57 VRVAIKKISPEHQYCCQRTLR-----IKILRFREHNIIGINDIRAPTIQMDVY 110
 QY 91 VWSRGTKDLDLSIFTTNTVYHSGDYCH--YRLLPFENYEHNTSVYK----- 141
 DB 111 I-----VQDLMETDLYLTLKTOHLSNDHICYFYQILRGKLYHSANVLRDLPKSNL 164
 QY 142 ----IHIEVNDKSGSACGCGPTVYTRRARWRDQAVDRGTGLCAMPANR-----PQGRAB 193
 DB 165 LNTTDDLKICDFGLARVDP--DH-----DHTGFLIEYVATRYRRAPEIMLN 209
 QY 194 GEGSSPSCPLQLM-----PLFLSSPRGQSMVPVHRSRGYRLCHLCMTS 240
 DB 210 SKGYTKS--IDWSVGCILAEWLSNRPIF-----PKGH-----YLDQNLHILGILG 253
 QY 241 G-----RCLLSLSOR--VVLGLP 256
 DB 254 SPSQEDLNLCIINLKARNYLLSLP 276

 RESULT 13
 Q91406
 ID 091406 PRELIMINARY; PRT; 202 AA.
 AC 091406;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE IPI.
 OS Salmo sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 NCBI_TaxID=8031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95279970; PubMed=7539051;
 RA Stratanm A., Jeserich G.,
 RT "Molecular cloning and tissue expression of a cDNA encoding IPI--a PO-
 RT like glycoprotein of trout CNS myelin."
 RL J. Neurochem. 64:2427-2436(1995).
 DR EMBL: S78261; AAB3439.1, -
 DR HSSP; P06907; INEU.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IGv_1.
 SQ SEQUENCE 202 AA; 22322 MW; 92C2900701B6E1B0 CRC64;

 Query Match 7.0%; Score 101.5; DB 13; Length 202;
 Best Local Similarity 23.5%; Pred. No. 0.052;
 Matches 35; Conservative 21; Mismatches 68; Indels 25; Gaps 4;

 QY 12 ALVSSACGCGVEVDESEAVY-----GMTFKILCISCRSEETNAETFTETPROK 62

Db 6 ALASVILLGIIVPQOSEAIVYTGEMERHALVGSIDIRLSCSPFSWMTSDVTFSS-WSYRPD 64
 QY 63 GTEEFVKILRYENEVLQLEEDERFEGRVVWNGSRGTDLQDLSTFTNTVYTNHSGDYECH 122
 Db 65 GARDALISIFHYAKGPYVDNKGPRDRLEFVGNPGR---DGSILLNLDYSDNGTFTCD 121
 QY 123 V-----YRLFFENYEHTSVV 139
 Db 122 AKNPDIWGRASSVRLVFEKVPYQAGVI 150

RESULT 14

Q14902 ID 014902 PRELIMINARY; PRT; 251 AA.

AC 014902; DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 GN Myelin protein zero.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RX MEDLINE=95135435; Pubmed=7530550;
 RA Rautenstrauss B., Nellis E., Grehl H., Pfeiffer R.A.,
 RT "Identification of a de novo insertional mutation in P0 in a patient
 RT with Dejerine-Sottas syndrome (DSS) phenotype."
 RL Hum. Mol. Genet. 3:1701-1702(1994).
 DR EMBL; Z31718; CAA83513.1; -.
 DR HSSP; P06907; INEU.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG; 1.
 SQ SEQUENCE 251 AA; 27950 MW; 6625C1C3CEF70E7D CRC64;

Query Match 6.8%; Score 98.5; DB 4; Length 251;
 Best Local Similarity 26.4%; Pred. No. 0.14;
 Matches 32; Conservative 23; Mismatches 61; Indels 5; Gaps 3;

QY 4 LLALVGAALV-SSACGGCVDSETEAVYGMTFKILICISCKRSEINAETFTMTFRQK 62
 Db 13 ILAVLFSLSLVSPAQALVYVTDREVGAVGSRVTLHCSEFWSSEWSDISFT-WRYQPE 71
 QY 63 GTEEFVKILRYENEVLQLEEDERFEGRVVWNGSRGTDLQDLSTFTNTVYTNHSGDYECH 122
 Db 72 GGRDAISIFHYAKGPYVDNKGPRDRLEFVGNPGR---DGSILLNLDYSDNGTFTCD 128
 QY 123 V 123
 Db 129 V 129

RESULT 15

Q9BR67 ID 09BR67 PRELIMINARY; PRT; 258 AA.

AC 09BR67; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;

RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC006491; AAH06491.1; -.
 DR HSSP; P06907; INEU.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003600; IG_1like.
 DR InterPro; IPR003606; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR00920; Myelin_P0.
 DR Pfam; PF00047; IG_1.
 DR PRINTS; PR00213; MYELINP0.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR SMART; SM00410; IG_1like; 1.
 DR PROSITE; PS00568; MYELIN_P0; 1.
 SQ SEQUENCE 258 AA; 28531 MW; 507A6AE23449E9D9 CRC64;

Query Match 6.8%; Score 98.5; DB 4; Length 258;
 Best Local Similarity 26.4%; Pred. No. 0.14;
 Matches 32; Conservative 23; Mismatches 61; Indels 5; Gaps 3;

QY 4 LLALVGAALV-SSACGGCVDSETEAVYGMTFKILICISCKRSEINAETFTMTFRQK 62
 Db 23 ILAVLFSLSLVSPAQALVYVTDREVGAVGSRVTLHCSEFWSSEWSDISFT-WRYQPE 81
 QY 63 GTEEFVKILRYENEVLQLEEDERFEGRVVWNGSRGTDLQDLSTFTNTVYTNHSGDYECH 122
 Db 82 GGRDAISIFHYAKGPYVDNKGPRDRLEFVGNPGR---DGSILLNLDYSDNGTFTCD 138
 QY 123 V 123
 Db 139 V 139

Search completed: January 29, 2003, 13:29:13
 Job time : 35 secs